

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 27, 2006, 01:48:32 ; Search time 178 Seconds
(without alignments)
1446.896 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIQSVWRQRYQSHPDAAVQ 556

Scoring table: BLQSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2941	100.0	556	3 US-09-771-161A-245
2	2941	100.0	556	4 US-10-190-012-1
3	2941	100.0	556	4 US-10-376-554-6
4	2941	100.0	556	4 US-10-704-921-14
5	2941	100.0	556	5 US-10-473-127-1372
6	2941	100.0	556	5 US-10-473-127-1373
7	2941	100.0	556	5 US-10-473-127-1374
8	2941	100.0	556	5 US-10-473-127-1377
9	2941	100.0	556	5 US-10-473-127-1378
10	2941	100.0	556	5 US-10-473-127-1380
11	2941	100.0	556	5 US-10-473-127-1382

; SEQ ID NO 245
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-245

Query Match 100.0%; Score 2941; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQSSSTPPGIPGGSRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQSSSTPPGIPGGSRQGPAMDGTAAEPRP 60

Oy 61 GAGSLQHAQPPQPKRKPDPFKFGKILGSGSPSTVVLARELATSREYAIKILKXHIK 120
Db 61 GAGSLQHAQPPQPKRKPDPFKFGKILGSGSPSTVVLARELATSREYAIKILKXHIK 120

Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDEKLYFGLSYAKGELLYIKIKGSPDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDEKLYFGLSYAKGELLYIKIKGSPDET 180

Oy 181 CTRPYTASIVSALEYLHGKGIIRDLKPNILLNEDMHQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGIIRDLKPNILLNEDMHQITDPTAKVLSPEKQARAN 240

Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300

Oy 301 PPEKFFPKARDLVEKLLVLDATKRLGCEMEGYPGLKAHPFESVTWENLHQTPPKLTA 360
Db 301 PPEKFFPKARDLVEKLLVLDATKRLGCEMEGYPGLKAHPFESVTWENLHQTPPKLTA 360

Oy 361 YLPAMSEDDDCYGNVNLISQPGCMQVSSSSSSHSLSASDTGLPQRSNGSIROYIHLD 420
Db 361 YLPAMSEDDDCYGNVNLISQPGCMQVSSSSSSHSLSASDTGLPQRSNGSIROYIHLD 420

Oy 421 SNSFELDLQFSEDKRLLEKQAGNPNHQPVENNLILOQGVDPKRGKLPARRQLLLE 480
Db 421 SNSFELDLQFSEDKRLLEKQAGNPNHQPVENNLILOQGVDPKRGKLPARRQLLLE 480

Oy 481 GPHLYYDVPNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTYYLADPSGNAHKCRKIQ 540
Db 481 GPHLYYDVPNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTYYLADPSGNAHKCRKIQ 540

Oy 541 EVMWRQRYQSHPDAAVQ 556
Db 541 EVMWRQRYQSHPDAAVQ 556

RESULT 2
US-10-190-012-1
; Sequence 1, Application US/10190012
; Publication No. US20030108971A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R

12	2941	100.0	556	5	US-10-473-127-1383	Sequence 1383, Ap
13	2941	100.0	556	5	US-10-473-127-1384	Sequence 1384, Ap
14	2941	100.0	556	5	US-10-723-860-2053	Sequence 2053, Ap
15	2941	100.0	556	5	US-10-689-576-1	Sequence 1, Appli
16	2941	100.0	556	5	US-10-509-599-28	Sequence 28, Appl
17	2838	96.5	535	5	US-10-473-127-1379	Sequence 1379, Ap
18	2682	91.2	506	5	US-10-473-127-1381	Sequence 1381, Ap
19	2202.5	74.9	468	5	US-10-473-127-1371	Sequence 1371, Ap
20	2202.5	74.9	468	5	US-10-473-127-1385	Sequence 1385, Ap
21	1900	64.6	361	4	US-10-664-421-106	Sequence 106, App
22	1900	64.6	361	5	US-10-941-635-107	Sequence 107, App
23	1710	58.1	319	5	US-10-473-127-1375	Sequence 1375, Ap
24	1710	58.1	319	5	US-10-473-127-1386	Sequence 1386, Ap
25	1486	50.5	285	4	US-10-217-574-13	Sequence 13, Appl
26	1486	50.5	285	4	US-10-217-555-13	Sequence 13, Appl
27	1237	41.7	238	3	US-09-771-161A-154	Sequence 154, App
28	1146.5	39.0	752	4	US-10-108-605-133	Sequence 133, App
29	1144.5	38.9	752	4	US-10-190-012-29	Sequence 29, Appl
30	1144.5	38.9	752	5	US-10-689-576-29	Sequence 29, Appl
31	1144.5	38.9	752	6	US-11-097-143-138	Sequence 138, App
32	1144.5	38.9	752	6	US-11-097-143-573	Sequence 573, App
33	1144.5	38.9	752	6	US-11-097-143-28173	Sequence 28173, A
34	1144.5	38.9	755	6	US-11-097-143-28170	Sequence 28170, A
35	973	33.1	539	6	US-11-097-143-28176	Sequence 28176, A
36	973	33.1	539	6	US-11-097-143-28179	Sequence 28179, A
37	940	32.0	636	3	US-09-205-658-160	Sequence 160, App
38	940	32.0	636	3	US-09-963-693-160	Sequence 160, App
39	935	31.8	632	3	US-09-205-658-159	Sequence 159, App
40	935	31.8	632	3	US-09-963-693-159	Sequence 159, App
41	917.5	31.2	473	4	US-10-369-493-13231	Sequence 13231, A
42	875.5	29.8	537	4	US-10-425-114-64801	Sequence 64801, A
43	872.5	29.7	537	4	US-10-425-114-67015	Sequence 67015, A
44	870.5	29.6	504	4	US-10-425-115-292727	Sequence 292727, A
45	846.5	28.8	628	4	US-10-369-493-22776	Sequence 22776, A

ALIGNMENTS

RESULT 1

US-09-771-161A-245
; Sequence 245, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0

TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Jaekle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,012
FILING DATE: 05-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 971253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Branen, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-190-012-1

Query Match 100.0%; Score 2941; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQSSSTPPGIPGGSRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQSSSTPPGIPGGSRQGPAMDGTAAEPRP 60

Oy 61 GAGSLQHAQPPQPKRKPDPFKFGKILGSGSPSTVVLARELATSREYAIKILKXHIK 120

Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Qy 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 3
US-10-376-554-6
; Sequence 6, Application US/10376554
; Publication No. US20030215849A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PDPK16 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-017C
; CURRENT APPLICATION NUMBER: US/10/376,554
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/361,196
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-554-6

Query Match 100.0%; Score 2941; DB 4; Length 556;

; PRIOR APPLICATION NUMBER: 60/424777
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-704-921-14

Query Match 100.0%; Score 2941; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Qy 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
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Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Qy 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 5
US-10-473-127-1372

Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Qy 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLILKMGVDPKRGKLFARRRQLLLE 480
Qy 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPMVKVLKGSIPWSQSLRPAKQKFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 4
US-10-704-921-14
; Sequence 14, Application US/10704921
; Publication No. US20040166099A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; TITLE OF INVENTION: MOLECULES PREFERENTIALLY ASSOCIATED WITH EFFECTOR T CELLS
; FILE REFERENCE: T1N-026CP
; CURRENT APPLICATION NUMBER: US/10/704,921
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/467477
; PRIOR FILING DATE: 2003-05-02

; Sequence 1372, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1372
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1372

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDQTAASPRP 60
Qy 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILSKRH1IK 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOGYPLKAHPFFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420

Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Db 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 6
US-10-473-127-1373
; Sequence 1373, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1373
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1373

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Qy 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120
Db 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1374
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1374

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Qy 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120
Db 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Qy 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Qy 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Db 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Qy 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Db 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Db 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 8
US-10-473-127-1377
; Sequence 1377, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:

Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Qy 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Qy 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Db 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Qy 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Db 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Db 481 GPHLYYVDPVNVKLGSIWMSQSLRPAKQPKTFVHTPNRTYYLMDPSGNAHKWCRKI 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 7
US-10-473-127-1374
; Sequence 1374, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041

; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1377
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1377

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSRQGPAMDGTAAAPRP 60
Qy 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120
Db 61 GAGSLQAQPPPPQPKRQPEDFKFGKILGSGSPSTVVLARELATSREYA1KILEKXHI1K 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLYIKIKIGSFDT 180
Qy 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGI1HRDLKPN1LLNEDMH1Q1TDPGTAKVLSPEKQARAN 240
Qy 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Db 241 SFVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPPFRAGNEYL1FOKI1KLEYD 300
Qy 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Db 301 PPEKFFPKARDLVEKLLVLDAATKRLGCEBMGYGPKAHPPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQRSGSNIQYIHDL 420

Oy 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Db 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Oy 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Db 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Oy 541 EVWRQRYQSHPDAAVQ 556
| | | | |
Db 541 EVWRQRYQSHPDAAVQ 556
| | | | |

RESULT 9
US-10-473-127-1378
; Sequence 1378, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zyco Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1378
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1378

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Oy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1380

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Oy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |
Oy 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Db 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Oy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Oy 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Db 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Oy 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Db 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Oy 541 EVWRQRYQSHPDAAVQ 556
| | | | |
Db 541 EVWRQRYQSHPDAAVQ 556
| | | | |

RESULT 11
US-10-473-127-1382
; Sequence 1382, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zyco Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01

Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |
Oy 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Db 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Oy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Oy 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Db 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Oy 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Db 481 GPHLYYVDVNVKVLKGEIPWSQSLRPAEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
| | | | |
Oy 541 EVWRQRYQSHPDAAVQ 556
| | | | |
Db 541 EVWRQRYQSHPDAAVQ 556
| | | | |

RESULT 10
US-10-473-127-1380
; Sequence 1380, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zyco Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1380
; LENGTH: 556

; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1382
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1382

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSMVKTQTSSSTPGIPGSGRQGPAMDGTAAERPR 60
| | | | |
Oy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
| | | | |
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSPDET 180
| | | | |
Oy 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Db 181 CTRFYTAIVSALEYLHGKIIHRDLKPENILLNEDMHIQITDGTAKVLSPEKQARAN 240
| | | | |
Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
| | | | |
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBGYGPKLKAHPFESVTWNLHQOTPPKLT 360
| | | | |
Oy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EGYIHDLD 420
| | | | |
Oy 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |
Db 421 SNSFELDLQPSSEDEKRLLLSKQAGGNPMHQPVENNLLKMGVVDKRGKLFARRRQLLLTE 480
| | | | |

Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 12

US-10-473-127-1383
; Sequence 1383, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1383
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1383

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60
Qy 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240

Db 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240
Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420
Qy 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480
Db 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480
Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 13

US-10-473-127-1384
; Sequence 1384, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1384
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1384

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60
Qy 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120

Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180

Qy 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240

Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300

Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360

Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420

Qy 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480
Db 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480

Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
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Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 14

US-10-723-860-2053
; Sequence 2053, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Azis, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2053
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2053

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSSTPPGIPGGSROGPAMDGTAAAPRP 60

Qy 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPQPRKRPDPFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120

Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDET 180

Qy 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKIIHRDLKPENILNEDMHQITDGTAKVLSPEKQARAN 240

Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYD 300

Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBEGYGPLKAHPFESVTWENLHOQTTPKLT 360

Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNI EGYIHDL 420

Qy 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480
Db 421 SNSFELDLOPSEDSKRLLEKQAGGNPMHQPVENNLI LKMGVDPKRGFLFARRRQLL 480

Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNKTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540

Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 15
US-10-689-576-1
: Sequence 1, Application US/10689576
: Publication No. US20050032185A1
: GENERAL INFORMATION:
: APPLICANT: Alessi, Dario R
: TITLE OF INVENTION: ENZYME
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
: STREET: 39 State Street
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14614-1310
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/689,576
: FILING DATE: 20-Oct-2003
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,667
: FILING DATE: 03-OCT-1997
: APPLICATION NUMBER: GB 9705462.1
: FILING DATE: 17-MAR-1997
: APPLICATION NUMBER: GB 9712826.8
: FILING DATE: 19-JUN-1997
: APPLICATION NUMBER: GB 9717253.0
: FILING DATE: 15-AUG-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Braman, Susan J
: REGISTRATION NUMBER: 34,103
: REFERENCE/DOCKET NUMBER: 07792.97R421
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 716-262-3640
: TELEFAX: 716-262-4133
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 556 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTTSOLYDAVP1QSSVVLCSGPCSPSMVKRTQTESSTPPG1PGGSRQGPAMDGTAAAPRP 60
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Db 61 GAGSLQHAQPPQPPQPRKRPEDFKFGKILGEGSPSTVVLARELATRSREYAIKILSKRHIIK 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQODEKLYPGLSYAKNGELLKYIRKIGSPDST 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQODEKLYPGLSYAKNGELLKYIRKIGSPDST 180
Qy 181 CTRPYTASIVSALEYLHGKDIHRDLKPENILLNEDWHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKDIHRDLKPENILLNEDWHIQITDPTAKVLSPEKQARAN 240
Qy 241 SPVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPFFRAGNSYLI FOKIIKLEYD 300
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Qy 301 FPKKFPKARDLVSKLLVLDATIKRLGCESEMGYGLQHPFFESVTWNLHQQTTPPKLTA 360
Db 301 FPKKFPKARDLVSKLLVLDATIKRLGCESEMGYGLQHPFFESVTWNLHQQTTPPKLTA 360
Qy 361 YLPAMSEDDSDCYGNVDNLLSQFCQVQVSSSSSSSLGASDTGLPQRSGSNISQYIHDL 420
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Qy 421 SNSFELDLQFSEDEKRLLESKQAGNPWHQFVENNLIJWGPVVDKRGFLFARRRQLLLTS 480
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Qy 481 GPHLYYVDPVNKLKGEI PMSQSLRPAKFNKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNKLKGEI PMSQSLRPAKFNKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

Search completed: June 27, 2006, 01:51:45
Job time : 180 secs

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:36:37 ; Search time 51 Seconds
(without alignments)
954.255 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIGVWRQRYQSHPDAAVQ 556

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2941	100.0	556	1 US-09-016-000-4	Sequence 4, Appli
2	2941	100.0	556	2 US-08-943-667-1	Sequence 1, Appli
3	2941	100.0	556	2 US-09-771-161A-245	Sequence 245, App
4	2937	99.9	556	2 US-09-156-793D-2	Sequence 2, Appli
5	1227	41.7	238	2 US-09-771-161A-154	Sequence 154, App
6	1144.5	38.9	752	2 US-08-943-667-29	Sequence 29, Appl
7	940	32.0	636	2 US-09-205-658-160	Sequence 160, App
8	935	31.8	632	2 US-09-205-658-159	Sequence 159, App
9	712	24.2	766	2 US-09-538-092-216	Sequence 216, App
10	655.5	22.3	901	2 US-09-248-796A-20495	Sequence 20495, A

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,000
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0465 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MMLR1D701
CLONE: 472480
US-09-016-000-4

Query Match 100.0%; Score 2941; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.4e+247;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVKTOTSSSTPPGIPGGSQGPAMDOTAAAPRP 60
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Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVKTOTSSSTPPGIPGGSQGPAMDOTAAAPRP 60
|||||
Qy 61 GAGSLQAQPPPPKRIKRPEDFKFKIKLGSFSTVVLARELATSREYA1KILKXHIK 120
|||||
Db 61 GAGSLQAQPPPPKRIKRPEDFKFKIKLGSFSTVVLARELATSREYA1KILKXHIK 120
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Qy 121 ENKVPVTRSDVMSRLDHPFFVKLYPTPDQDEKLYPGLSYANGLKLYIRKIGSPDST 180
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Db 121 ENKVPVTRSDVMSRLDHPFFVKLYPTPDQDEKLYPGLSYANGLKLYIRKIGSPDST 180
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Qy 181 CTRPYTATISALEYLGKGI1HRDLKPENILLNEDMI1QITDPTAKVLSPPSKQARAN 240
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Db 181 CTRPYTATISALEYLGKGI1HRDLKPENILLNEDMI1QITDPTAKVLSPPSKQARAN 240
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11	614	20.9	113	2	US-09-205-658-173	Sequence 173, App
12	573	19.5	104	2	US-09-205-658-202	Sequence 202, App
13	571.5	19.4	420	2	US-09-949-016-11701	Sequence 11701, A
14	562	19.1	431	2	US-09-031-295-2	Sequence 2, Appli
15	562	19.1	431	2	US-10-000-039-2	Sequence 2, Appli
16	561	19.1	407	2	US-10-067-977-4	Sequence 4, Appli
17	561	19.1	445	2	US-10-067-977-2	Sequence 2, Appli
18	561	19.1	526	2	US-10-094-749-1861	Sequence 1861, Ap
19	560.5	19.1	256	2	US-09-964-956-72	Sequence 72, Appl
20	560.5	19.1	358	2	US-09-949-016-6582	Sequence 6582, Ap
21	560.5	19.1	358	2	US-10-427-923-4	Sequence 4, Appli
22	556	18.9	398	2	US-09-538-092-501	Sequence 501, App
23	556	18.9	398	2	US-09-487-5588-404	Sequence 404, App
24	555	18.9	430	1	US-08-712-709-9	Sequence 9, Appli
25	555	18.9	430	2	US-09-111-444-9	Sequence 9, Appli
26	555	18.9	430	2	US-09-541-228-9	Sequence 9, Appli
27	554	18.8	380	2	US-09-487-5588-402	Sequence 402, App
28	553	18.8	431	1	US-08-712-709-5	Sequence 5, Appli
29	553	18.8	431	2	US-09-111-444-5	Sequence 5, Appli
30	553	18.8	431	2	US-09-541-228-5	Sequence 5, Appli
31	550.5	18.7	350	2	US-09-538-092-991	Sequence 991, App
32	550.5	18.7	359	2	US-09-949-016-7862	Sequence 7862, Ap
33	543	18.5	343	2	US-09-394-455-15	Sequence 15, Appl
34	542	18.4	336	2	US-09-394-455-2	Sequence 2, Appli
35	542	18.4	343	2	US-09-394-455-34	Sequence 34, Appl
36	542	18.4	350	2	US-09-538-092-946	Sequence 946, App
37	542	18.4	351	2	US-09-394-455-4	Sequence 4, Appli
38	542	18.4	351	2	US-09-771-161A-194	Sequence 194, App
39	540	18.4	343	2	US-09-394-455-38	Sequence 38, Appl
40	540	18.4	595	2	US-09-417-197-69	Sequence 69, Appl
41	539.5	18.3	541	2	US-09-205-658-154	Sequence 154, App
42	538	18.3	350	2	US-09-457-040B-37	Sequence 37, Appl
43	538	18.3	351	2	US-09-457-040B-6	Sequence 6, Appli
44	537	18.3	260	1	US-07-857-224B-4	Sequence 4, Appli
45	535.5	18.2	637	2	US-09-817-310-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-016-000-4
; Sequence 4, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

Db 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPFRAGNEYLI1FKI1KLEYD 300
Qy 301 PFEKFFPKARDLVEKLLVLQDITKRLGCEEMGYGLKHAFFPFSVTWNLHQOTPKPKTA 360
|||||
Db 301 PFEKFFPKARDLVEKLLVLQDITKRLGCEEMGYGLKHAFFPFSVTWNLHQOTPKPKTA 360
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Db 481 GPHLYYDVPNVKVLKGSIPMSQSLRPEAKNFKTFVPHVTPNRTTYLMDPSNAHGWCRKIQ 540
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Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556
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RESULT 2
US-08-943-667-1
; Sequence 1, Application US/08943667
; Patent No. 6734001
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R
; TITLE OF INVENTION: ENZYMS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Jaechle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 971253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:

NAME: Brennan, Susan J
REGISTRATION NUMBER: 34,103
REFERENCES/DOCKET NUMBER: 87792, 97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-943-667-1

Query Match 100.0%; Score 2941; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.4e-247;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Oy 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
Db 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
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Db 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIROYIHDL 420
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Db 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIROYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIROYIHDL 420
Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIQMGPDVKRGLFARRRQLLLTE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIQMGPDVKRGLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGSIPWSQSLRPAENKFTFFVHTPNRTTYLMDPSGNAHKWCRKI 540
Db 481 GPHLYYVDPVNKLKGSIPWSQSLRPAENKFTFFVHTPNRTTYLMDPSGNAHKWCRKI 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 4
US-09-156-793D-2
Sequence 2, Application US/09156793D
Patent No. 6682920
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Philip T.
APPLICANT: Stokoe, David
TITLE OF INVENTION: Compositions and Methods for Identifying PKB Kinase
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: 1030-US
CURRENT APPLICATION NUMBER: US/09/156,793D
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/060,190
PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 2
LENGTH: 556
TYPE: PRT
ORGANISM: PKB Kinase
US-09-156-793D-2

Query Match 99.9%; Score 2937; DB 2; Length 556;
Best Local Similarity 99.8%; Pred. No. 3.2e-247;
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Oy 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
Db 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKGSELLKYIRKIGSPDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKGSELLKYIRKIGSPDET 180

Db 481 GPHLYYVDPVNKLKGSIPWSQSLRPAENKFTFFVHTPNRTTYLMDPSGNAHKWCRKI 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 3
US-09-771-161A-245
Sequence 245, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patent In version 3.0
SEQ ID NO: 245
LENGTH: 556
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-245

Query Match 100.0%; Score 2941; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.4e-247;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVRTQTSSSTPPGIPGSGRQGPAMDGTAAAPRP 60
Oy 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
Db 61 GAGSLQHAQPPPPQPRKCRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKGSELLKYIRKIGSPDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDEKLYFGLSYAKGSELLKYIRKIGSPDET 180
Oy 181 CTRFYTTARIVSALEYLHGKGIHRLDKPENILLNEDMHQITDFTGTAKVLSPEKQARAN 240
Db 181 CTRFYTTARIVSALEYLHGKGIHRLDKPENILLNEDMHQITDFTGTAKVLSPEKQARAN 240
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIILKLYD 300
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIILKLYD 300
Oy 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360

Oy 181 CTRFYTTARIVSALEYLHGKGIHRLDKPENILLNEDMHQITDFTGTAKVLSPEKQARAN 240
Db 181 CTRFYTTARIVSALEYLHGKGIHRLDKPENILLNEDMHQITDFTGTAKVLSPEKQARAN 240
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIILKLYD 300
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIILKLYD 300
Oy 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDTATKRLGCEMSEGYGLKAHPFESVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIROYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIROYIHDL 420
Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIQMGPDVKRGLFARRRQLLLTE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIQMGPDVKRGLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGSIPWSQSLRPAENKFTFFVHTPNRTTYLMDPSGNAHKWCRKI 540
Db 481 GPHLYYVDPVNKLKGSIPWSQSLRPAENKFTFFVHTPNRTTYLMDPSGNAHKWCRKI 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 5
US-09-771-161A-154
Sequence 154, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patent In version 3.0
SEQ ID NO: 154
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-154

Query Match 41.7%; Score 1227; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 9.6e-99;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

1 TELEFAX: 716-262-4133
2 INFORMATION FOR GEO ID NO: 29:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 752 amino acids
5 TYPE: amino acid
6 STRANDEDNESS: single
7 TOPOLOGY: linear
8 MOLECULE TYPE: protein
9 HYPOTHETICAL: NO
10 ANTI-SENSE: NO
11 ORIGINAL SOURCE:
12 ORGANISM: Drosophila
13 US-98-941-667-29

```

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1  RESULT 6
2  US-08-943-667-29
3
4  : Sequence 29, Application US/08943667
5  : Patent No. 6734001
6
7  : GENERAL INFORMATION:
8
9  : APPLICANT: Alessi, Dario R
10 :
11 : TITLE OF INVENTION: ENZYME
12 :
13 : NUMBER OF SEQUENCES: 35
14 :
15 : CORRESPONDENCE ADDRESS:
16
17 : ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
18 :
19 : STREET: 39 State Street
20 :
21 : CITY: Rochester
22 :
23 : STATE: New York
24 :
25 : COUNTRY: USA
26 :
27 : ZIP: 14614-1310
28
29 : COMPUTER READABLE FORM:
30
31 : MEDIUM TYPE: Floppy disk
32 :
33 : COMPUTER: IBM PC compatible
34 :
35 : OPERATING SYSTEM: PC-DOS/MS-DOS
36 :
37 : SOFTWARE: PatentIn Release #1.0, Version #1.30
38
39 : CURRENT APPLICATION DATA:
40
41 : APPLICATION NUMBER: US/08/943,667
42 :
43 : FILING DATE: 03-OCT-1997
44 :
45 : CLASSIFICATION: 435
46 :
47 : PRIOR APPLICATION DATA:
48
49 : APPLICATION NUMBER: GB 9705462.1
50 :
51 : FILING DATE: 17-MAR-1997
52 :
53 : PRIOR APPLICATION DATA:
54
55 : APPLICATION NUMBER: GB 9712826.8
56 :
57 : FILING DATE: 19-JUN-1997
58 :
59 : PRIOR APPLICATION DATA:
60
61 : APPLICATION NUMBER: GB 9717253.0
62 :
63 : FILING DATE: 15-AUG-1997
64 :
65 : ATTORNEY/AGENT INFORMATION:
66
67 : NAME: Brennan, Susan J
68 :
69 : REGISTRATION NUMBER: 34,103
70 :
71 : REFERENCE/DOCKET NUMBER: 87792.97R421
72 :
73 : TELECOMMUNICATION INFORMATION:
74
75 : TELEPHONE: 716-262-1640

```

[illegible]

```

Db      349 PSTRITQS-----LMAKGFENVDWVNIANKPPVLAHYPATPGPSE-----YYSNIG 398
Qy      380 ----LSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNI EQ---YIHDLDSNSFELDQF 430
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      399 PVFGLDRLAFRLANLGHIDASASQPTFRP-----GNVEHRCQPVVSEIAPRA-----N 448
Qy      431 SEDEKRL-----LEKQAGNPMHQFVENNLLIKMGPDVKRGLFARRQQLLLTEGPHLY 485
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      449 SBAEKRAARAQKLSEORVKNPFHPTNSNLLIKQOYLEKRGGLFARRMPLLTGPHILL 508
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      486 YVDVNVKVLKGSIPWSQELRPAKNGKFTFVVIHTPNRTYLLMDPSGNAHMKCRKIQEVRQ 545
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      509 YIDVNVVLKQGEVPTPCMQVLEKNGSTFTFHTPNRVYLLPDLKEKADSWCKAIINDV-RK 567
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      546 RY 547
          ||
Db      548 RY 569

```

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> RESULT 8
> US-09-205-658-159
> Sequence 159, Application US/09205658
> Patent No. 6861256
> GENERAL INFORMATION:
> APPLICANT: Ruvkun, Gary
> APPLICANT: Osg, Scott
> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
> TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
> FILE REFERENCE: 00786/351004
> CURRENT APPLICATION NUMBER: US/09/205,658
> CURRENT FILING DATE: 1998-12-03
> EARLIER APPLICATION NUMBER: 08/857,076
> EARLIER FILING DATE: 1997-05-15
> EARLIER APPLICATION NUMBER: 08/888,534
> EARLIER FILING DATE: 1997-07-07
> EARLIER APPLICATION NUMBER: US98/10080
> EARLIER FILING DATE: 1998-05-15
> NUMBER OF SEQ ID NOS: 328
> SOFTWARE: PstSeq for Windows Version 4.0
> SEQ ID NO 159
> LENGTH: 632
> TYPE: CDS
> ORGANISM: Caenorhabditis elegans
> US-09-205-658-159

```

```

RESULT 7
US-09-205-658-160
; Sequence 160, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PfastSEQ for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-160

```

Query Match 32.0%; Score 940; DB 2; Length 636;
Best Local Similarity 36.9%; Pred. No. 4.2e-73;
Matches 200; Conservative 101; Mismatches 159; Indels 82; Gaps 11.

Qy	62	AGSLQAHPPPQPKRKRPFDFKPGKILGEGSFSTVVLARELATSREYAIKILSKRHHIKE	121
Db	54	AKSIKEGCP-----KRTSDMPFLQSGHGGAISGVFRCSVATAAMFAVKKLQSYLAIRH	108
Qy	122	NKVPVYVTRERDVSRLD-----HPFFVLYLFTFODDEKILFGLSYAKNGELLYKIRKIGS	176
Db	109	QMDAIIRSKNILLTYSQCGGHPVTVTLTTHFDQAIRVYFVIGLVENKDLGSSLCFHS	168
Qy	177	PDSTCTRPYTAIRVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPOTAKVLIS-----	231
Db	169	FDMLTSKFPASSILTLOLFDHNKIVHRDNKPDNVLIKQDGHILITDPGSAQAFOGLQLS	228
Qy	232	-----PESKQARANSFVOTAYVSEPLLTEKSAK	260
Db	229	QEPTDANQASSRSDDSGSPPTTRFYSDSEVPSENTAARTFTVGTALVSEPMKLDGDDVO	288
Qy	261	KSSDLWALGCIITVQLVAGLPPFRAGNEVYLFQIKLSEYSPGPPFKARDLVFLVKLI	320
Db	269	POTDIWGLCILLFQCLAQGPPFRVAVNQHLLKRIQSLDSPFSGPPSEASSIIAKILVRD	348
Qy	321	ATNRLGCEBNGSGPLKRAHPFSEVTNENHIOOTPKPLTAYLPAMSEDDSDCYGNLDL	379

Query Match 31.8%; Score 935; DB 2; Length 632;
Best Local Similarity 37.2%; Pred. No. 1.1e-72;
Matches 202; Conservative 101; Mismatches 152; Indels 88; Gaps 13;

[illegible]

Qy 177 FOSTCTRTFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVL----- 230
Db 169 FOMLTSTKFFASSILTLGLPLANDKIVHRDMKPDNVLQKQGHILITDPSGAQAPGGLQLS 228
Qy 231 -----SP-----SKQARANSFVGTAAQYVSPPELLTEKSACKS 262
Db 229 QEGPTDANQASSRSSDGGSPPTFRFYGDSSEENTARTTTPVGTALVSPENLADGDVGPQ 288
Qy 263 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 322
Db 289 TDIMGLGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 348
Qy 323 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAEMSEDDDCYGNVHL 379
Db 349 TRITSQ-----LMAHKFFENVDMVNIANIKPPVLHAYIPATPGEP-----YTSNIGPV 398
Qy 380 -----LSQFGCMQVSSSSSSSHLSASDTGLPQRSNIEQ-----YIHDLSNSFELDQ 429
Db 399 EPGLDLRLFRNLNGLNDA-----SASOPSTP-----SNVEHGDPPVSEIAPRA----- 443
Qy 430 FSEDEKRL-----LEKQAGGNPMHOFVNNLILKMGPMVDKRGKLFARRRQLLLTEGPHL 484
Db 444 NSBASKNRAARAQKLSQRVKNPFIPTNNSLILKQGYLKKKGLFARRRMFLTEGPHL 503
Qy 485 YYVDVNVKVLKGEIPWSQSLRPSAKNFKTFVHTPNRTYTLMDPSGNAHKWCKRIQVSWR 544
Db 504 LYIDVNVKVLKGEIPWTPQMVBLNSGTFPIHTPNRYVTLFDEKKADWCKAINDR-V 562
Qy 545 QRY 547
Db 563 KRY 565

RESULT 9
US-09-538-092-216
; Sequence 216, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurePatSeqFormatter Version 0.9
; SEQ ID NO 216
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURES:
; NAME/KEY: misc_feature

; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YDR490C
US-09-538-092-216

Query Match 24.2%; Score 712; DB 2; Length 766;
Best Local Similarity 30.3%; Pred. No. 4.1e-53;
Matches 187; Conservative 87; Mismatches 154; Indels 190; Gaps 15;

Qy 27 SMVRTQTSSTTTPGIPGDSRQ-----PAMDGT-----AASPRPQAGSLQH 67
Db 22 SASHTQTQSYPRFPVVGSSNSQSGSELQASPOGQFGSKALTSNRPIPLANDDPG---MQH 78
Qy 68 AQP-PPQPRKGRPE-----DPKFGKILGEGSFST 95
Db 79 EMLGDPKRRRRSSMAERGAAKIVKQVDPATGELTHGVKMGIKDFKPGQLADGQSYSS 138
Qy 96 VVLARELATSREYAIIKLEKRHIIKENKVPYVTRERDVMSRLDHPFFV-KLYPTFQDDEK 154
Db 139 VVLATARDSQKCYAVKVLKSKYLIROKKVKYVTVKALQKLKNGTKGIFKLPTFDQRA 198
Qy 155 LYFGLSYAKNGELLYKIRKIGSPDSTCTRTFYTAIVSALSYLHGKGIHRLDKPENILLN 214
Db 199 LYFLLAYAPHODFLGLIKKYGSLNSTCARYYASQIIDAVDSLHNIIGIHRD:KVENILLD 258
Qy 215 EDHIIQITDPTAKVLSPEKQ-----ARANSFVGTAAQYVSPPELLTEKSACKS 263
Db 259 IQMKVKLTDPTAKILPEPSNTADGKPYFDLYAKSKSFVGTAEYVSPPELLADNYTDSRC 318
Qy 264 DLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 322
Db 319 DINAPGCIYQMLAGKPPFAANEYLTFOVKMKIQTATAGFPQIVKDLVKLLVLDPND 378
Qy 324 RLGCSEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAY-----LPAMSEDD--- 369
Db 379 RLTIQ-----IKHLFFHEVNFEDGSDVNDNPPBIQYKINAEAMKPLQKVSSTTV 432
Qy 370 -----EDC 372
Db 433 IQANLQLAGNHADTFLQAPATSQERSVIGMTAATAAFNKDYTSOPKLGSKSSTVSRA 492
Qy 373 YGNYDNLSQFGCMQVSSSSSSSHLSASDTGLPQRSNIEQ-----YIHDLSNSFELDQ 429
Db 493 SNNTDREVIQKCVSKNRASVSSPSTSTSRGKNRSRSDAPWSRYLQND----- 543
Qy 430 FSEDEKRLLEKQAG-----GNPMHOFVNNLILKMGPMVDKRGKLFARRRQLLLTEGPHL 469
Db 544 -----SRVLMKREVALSTRNLESDPVGLNVALDYKNP-----LDIEPTDSAGK 588
Qy 470 FARRRQLLTEGPHLYV 487
Db 589 FYKMFLLITNLGRALVFV 606

RESULT 10
US-09-248-796A-20495
; Sequence 20495, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20495
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20495

Query Match 22.3%; Score 655.5; DB 2; Length 901;
Best Local Similarity 37.1%; Pred. No. 4.4e-48;
Matches 144; Conservative 69; Mismatches 116; Indels 59; Gaps 10;

Qy 59 RPGAGSLQHAQPPPO-----RKGRPEDFKFGKILGEGSFVTLARELATSREYA 109
Db 53 QPSNRSTQOOQNTSQOSQSLAAKRRSARDYOPGAKIGEGSYSTYSALDKYTNRTYA 112
Qy 110 IKILEKRHIIKENKVPYVTRERDVMSRL--DHPPFVKLYPTFQDDEKLYPGLSYAKNGEL 167
Db 113 IKVLSKRHIVKENKIKYVNIKTTLNRLGQOHGPIVQLYTTQDSSSFFVLDPAHYGEL 172
Qy 168 LKVIKIRKIGSPDSTCTRTFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTA 227
Db 173 LSIIRKPGSLSSSVLKPFYMQIIDAIVRPIHLKGVHRDLKPENILVGHDFNLKITDPGA 232
Qy 228 KVL-----SPE-SKQARANSFVGTAAQYVSPPELLTEKSACKSSDLMAL 268
Db 233 KLLGNHSEPNKEKIDYNSVDASPEVSDTRKGSFVGTAEYVSPPELLNINICOFESDIWAI 292
Qy 269 GCIIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 326
Db 293 GCILYQFFNVPVPPGKSTYLTFSKIIINVDSYKSPILPLPPOVLIQIDLILSRSPARAT 352
Qy 327 CEMEGYGLKHAHPFFSVTWENLHOOTPPKLTAY-----LPAMSEDDDCYGN 375
Db 353 IPH-----IMSRMFSIDPDDQNTIMHRKVPFRFAAGAITPSPAMPPOHGN-----OT 401
Qy 376 YDNLSQFGCMQVSSSSSSSHLSASDTG 403
Db 402 NRNVNKSYSYTHQLQS-----QILASEG 424

RESULT 11
US-09-205-658-173
; Sequence 173, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus or Homo sapiens
US-09-205-658-173

Query Match 20.9%; Score 614; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 8.4e-46;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 322
Db 1 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFFPKFPPKARDLVEKLLVLDA 60
Qy 323 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAEMSEDDDCYGN 375
Db 61 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAEMSEDDDCYGN 113

RESULT 12
US-09-205-658-202
; Sequence 202, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 104
; TYPE: PRT

Search completed: June 27, 2006, 01:38:02
Job time : 53 secs

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:28:03 ; Search time 298 Seconds
(without alignments)
1725.868 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIGVQRQYQSHDAAVQ 556

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_7.2.*
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2941	100.0	556	1	PDPK1_HUMAN	O15530 homo sapien
2	2941	100.0	556	2	Q6P120_HUMAN	Q6P120 homo sapien
3	2926	99.5	556	2	Q53HJ9_HUMAN	Q53HJ9 homo sapien
4	2787.5	94.8	559	1	PDPK1_RAT	O55173 rattus norv
5	2769.5	94.2	559	1	PDPK1_MOUSE	Q92280 mus musculu
6	2764.5	94.0	559	2	Q3UWZ0_MOUSE	Q3UWZ0 mus musculu
7	2758.5	93.8	559	2	Q3UGN6_MOUSE	Q3UGN6 mus musculu
8	2732.5	92.9	551	2	Q81024_MOUSE	Q81024 mus musculu
9	2626.5	89.3	532	2	Q8K1L3_MOUSE	Q8K1L3 mus musculu
10	2626.5	89.3	556	2	Q5F3U4_CHICK	Q5F3U4 gallus gall
11	2560.5	87.1	522	2	Q3TRL2_MOUSE	Q3TRL2 mus musculu
12	2391.5	81.3	558	2	Q4S4R0_TETNG	Q4S4R0 tetradon n
13	2336	79.4	492	2	Q59EH6_HUMAN	Q59EH6 homo sapien
14	2228	75.8	537	2	Q6NZV1_BRARE	Q6NZV1 brachydanio
15	2202.5	74.9	429	2	Q9BRD5_HUMAN	Q9BRD5 homo sapien

RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=98035195; PubMed=9368760; DOI=10.1016/S0960-9822(06)00336-8;
RA Alessi D.R., Deak M., Casamayor A., Caudwell F.B., Morrice N.A.,
RA Norman D.G., Gaffney P.R.J., Reese C.B., MacDougall C.N., Harbison D.,
RA Ashworth A., Bonnes M.;
RT "3-phosphoinositide-dependent protein kinase-1 (PDK1): structural and
RT functional homology with the Drosophila DSTPK61 kinase.";
RL Curr. Biol. 7:776-789(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3).
RC TISSUE=Myeloid;
RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;
RA Stephens L.R., Anderson K.B., Stokoe D., Brdjunent-Bromage H.,
RA Painter G.F., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,
RA Tempest P., Coadwell W.J., Hawkins P.T.;
RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-
RT trisphosphate-dependent activation of protein kinase B.";
RL Science 279:710-714(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywicki M.T., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP MUTAGENESIS OF ARG-474, AND ALTERNATIVE SPLICING.
RX MEDLINE=98301766; PubMed=9637919; DOI=10.1016/S0960-9822(98)70274-X;
RA Anderson K.B., Coadwell W.J., Stephens L.R., Hawkins P.T.;
RT "Translocation of PDK-1 to the plasma membrane is important in
RT allowing PDK-1 to activate protein kinase B.";
RL Curr. Biol. 8:684-691(1998).
RN [6]
RP PHOSPHORYLATION SITES SER-25; SER-241; SER-393; SER-396 AND SER-410,
RP AND MUTAGENESIS OF SER-25; SER-241; SER-393; SER-396 AND SER-410.
RX MEDLINE=99386657; PubMed=10455013; DOI=10.1042/0264-6021.3420287;
RA Casamayor A., Morrice N.A., Alessi D.R.;
RT "Phosphorylation of Ser-241 is essential for the activity of 3-
RT phosphoinositide-dependent protein kinase-1: identification of five

16	2093.5	71.2	434	2	Q3UEW8_MOUSE	Q3UEW8 mus musculu
17	1931	65.7	367	2	Q9UPJ6_HUMAN	Q9UPJ6 homo sapien
18	1826	62.1	396	2	Q6A1A2_HUMAN	Q6A1A2 homo sapien
19	1710	58.1	319	2	Q9UPJ7_HUMAN	Q9UPJ7 homo sapien
20	1622.5	55.2	571	2	Q76BX2_ASTPE	Q76BX2 asterina pe
21	1431	48.7	822	2	Q9BMK6_APLCA	Q9BMK6 aplysia cal
22	1144.5	38.9	836	1	PDPK1_DROME	Q9w0v1 drosophila
23	1027	34.9	484	2	Q7PUX5_ANOGA	Q7PUX5 anopheles g
24	940	32.0	636	1	PDPK1_CABEL	Q9y1j3 caenorhabdi
25	939	31.9	813	2	Q5B8M0_EHEND	Q5B8M0 aspergillus
26	930	31.6	686	2	Q54TW2_DICDI	Q54TW2 dictyosteli
27	928	31.6	850	2	Q2UBU7_ASOPU	Q2UBU7 aspergillus
28	908.5	30.9	839	2	Q4WUD7_ASOPU	Q4WUD7 aspergillus
29	903	30.7	630	2	Q5WNC4_CABER	Q5WNC4 caenorhabdi
30	873.5	29.7	592	1	KSG1_SCHPO	Q12701 schizosacch
31	868.5	29.5	812	2	Q4HWD3_GIBZE	Q4HWD3 gibberella
32	868.5	29.5	922	2	Q873K1_NEUCR	Q873K1 neurospora
33	832.5	28.3	1542	2	Q6CFM7_YARLI	Q6cfm7 yarrowia li
34	832	28.3	488	2	Q9LZ74_ARATH	Q9LZ74 arabidopsis
35	832	28.3	491	2	Q9XF67_ARATH	Q9xf67 arabidopsis
36	821	27.9	498	2	Q8RUE8_ORYSA	Q8rue8 oryza sativ
37	820	27.9	483	2	Q9SQY4_ARATH	Q9sqy4 arabidopsis
38	820	27.9	486	2	Q4V3C8_ARATH	Q4v3c8 arabidopsis
39	816.5	27.8	494	2	Q516E8_LYCSB	Q516E8 lycopersico
40	800	27.2	908	2	Q54PK9_DICDI	Q54pk9 dictyosteli
41	795.5	27.0	1062	2	Q6B1K8_DESHA	Q6b1k8 debaryomyce
42	763.5	26.0	944	2	Q5A3P6_CANAL	Q5a3p6 candida alb
43	760.5	25.9	1153	2	Q5A3V9_CANAL	Q5a3v9 candida alb
44	748.5	25.5	1081	1	KOKO_YEAST	Q12236 saccharomyc
45	733	24.9	408	2	Q3B9L6_ARATH	Q3b9l6 arabidopsis

ALIGNMENTS

RESULT 1

PDPK1_HUMAN

ID PDPK1_HUMAN STANDARD; PRT; 556 AA.
AC O15530;
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1998, sequence version 1.
DT 07-MAR-2006, entry version 58.
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (hPDK1).
GN Name=PDPK1; Synonyms=PDK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=97250749; PubMed=9094314; DOI=10.1016/S0960-9822(06)00122-9;
RA Alessi D.R., James S.R., Downes C.P., Holmes A.B., Gaffney P.R.J.,
RA Reese C.B., Cohen P.;
RT "Characterization of a 3-phosphoinositide-dependent protein kinase
RT which phosphorylates and activates protein kinase B alpha.";
RL Curr. Biol. 7:261-269(1997).

RT sites of phosphorylation in vivo.";
RL Biochem. J. 342:287-292(1999).
RN [7]
RP MUTAGENESIS OF ALA-277.
RX MEDLINE=99392684; PubMed=10364160;
RA Paradis E., Allison M., Toker A., Thomas J.H., Ruvkun G.;
RT "A PDK1 homolog is necessary and sufficient to transduce AGE-1 PI3
RT kinase signals that regulate diapause in Caenorhabditis elegans.";
RL Genes Dev. 13:1438-1452(1999).
RN [8]
RP PHOSPHORYLATION SITES TYR-9; SER-241; TYR-373 AND TYR-376, AND
RP MUTAGENESIS OF TYR-9; TYR-373 AND TYR-376.
RX MEDLINE=21463095; PubMed=11481331; DOI=10.1074/jbc.M105916200;
RA Park J., Hill M.M., Hess D., Brazil D.P., Hofsteenge J.,
RA Hemmings B.A.;
RT "Identification of tyrosine phosphorylation sites on 3-
RT phosphoinositide-dependent protein kinase-1 (PDK1) and their role in
RT regulating kinase activity.";
RL J. Biol. Chem. 276:37459-37471(2001).
RN [9]
RP PHOSPHORYLATION SITE SER-241.
RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
RA Beaulieu S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in
CC signaling processes and in development (By similarity). Isoform 3
CC is catalytically inactive.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
CC cell stimulation leading to its translocation. Tyrosine
CC phosphorylation seems to occur only at the plasma membrane.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O15530-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O15530-2; Sequence=VSP_004894;
CC Name=3;
CC IsoId=O15530-3; Sequence=VSP_004895;
CC -1- TISSUE SPECIFICITY: Appears to be expressed ubiquitously.
CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.
CC Phosphorylation on Ser-241 in the activation loop is required for
CC full activity. PDK1 itself can autophosphorylate Ser-241, leading
CC to its own activation.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AF017995; AAC51825.1; -; mRNA.
DR EMBL; Y15056; CAA75341.1; -; mRNA.
DR EMBL; BC012103; AAH12103.1; -; mRNA.

DR PDB: 1H1W; X-ray; A=71-359.
 DR PDB: 1OKY; X-ray; A=51-360.
 DR PDB: 1OKZ; X-ray; A=51-360.
 DR PDB: 1UJ3; X-ray; A=51-360.
 DR PDB: 1UJ7; X-ray; A=51-360.
 DR PDB: 1UJ8; X-ray; A=51-360.
 DR PDB: 1UJ9; X-ray; A=72-357.
 DR PDB: 1UVR; X-ray; A=71-359.
 DR PDB: 1W1D; X-ray; A=409-556.
 DR PDB: 1W1G; X-ray; A=409-556.
 DR PDB: 1W1H; X-ray; A/B/C/D=409-556.
 DR PDB: 1Z5M; X-ray; A=74-359.
 DR PDB: 2B1Y; X-ray; A=51-360.
 DR Ensembl: ENSG00000140992; Homo sapiens.
 DR H-invdb: HIX0012732; .
 DR HGNC: HGNC:6816; PDPK1.
 DR MIM: 605213; gene.
 DR LinkHub: O15530; .
 DR GO: GO:0005737; C:cytoplasm; IEP.
 DR GO: GO:0005886; C:plasma membrane; IEP.
 DR GO: GO:0004676; P:3-phosphoinositide-dependent protein kinase. . .; TAS.
 DR GO: GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
 DR GO: GO:0008286; P:insulin receptor signaling pathway; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR011993; PH_type.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS50003; PH_DOMAIN; FALSE_NEG.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW 3D-structure; Alternative splicing; ATP-binding; Kinase; Membrane;
 KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
 KW Transferase.
 FT CHAIN 1 556 3-phosphoinositide-dependent protein
 FT kinase 1.
 FT /FTId=PRO_000006500.
 FT DOMAIN 82 342 Protein kinase.
 FT DOMAIN 459 550 PH.
 FT NP_BIND 68 96 ATP (By similarity).
 FT COMPBIAS 369 398 Poly-Ser.
 FT ACT_SITE 205 205 Proton acceptor (By similarity).
 FT BINDING 111 111 ATP (By similarity).
 FT MOD_RES 9 9 Phosphotyrosine.
 FT MOD_RES 25 25 Phosphoserine.
 FT MOD_RES 241 241 Phosphoserine (by autocatalysis).
 FT MOD_RES 373 373 Phosphotyrosine.
 FT MOD_RES 376 376 Phosphotyrosine.
 FT MOD_RES 393 393 Phosphoserine.
 FT MOD_RES 396 396 Phosphoserine.
 FT MOD_RES 410 410 Phosphoserine.

FT VARSPLIC 1 50 Missing (in isoform 2).
 FT VARSPLIC 238 263 /FTId=VSP_004894.
 FT VARSPLIC 238 263 Missing (in isoform 3).
 FT MUTAGEN 9 9 /FTId=VSP_004895.
 FT MUTAGEN 25 25 Y->F: Slight reduction in pervanadate-
 FT MUTAGEN 241 241 stimulated tyrosine phosphorylation.
 FT MUTAGEN 277 277 S->A: No effect.
 FT MUTAGEN 241 241 S->A: No activation.
 FT MUTAGEN 277 277 A->V: 3-fold increase in kinase activity.

Query Match 100.0%; Score 2941; DB 1; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3.5e-184;
 Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGGSROGPAMDGTAAEPRP 60
 Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGGSROGPAMDGTAAEPRP 60
 Oy 61 GAGSLQHAQPPPPQPKRKPDPKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
 Db 61 GAGSLQHAQPPPPQPKRKPDPKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
 Oy 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180
 Db 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180
 Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQIOTDPTAKVLSPEKQARAN 240
 Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQIOTDPTAKVLSPEKQARAN 240
 Oy 241 SFVGTAAQVSPPELLTEKSACKSSDLALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
 Db 241 SFVGTAAQVSPPELLTEKSACKSSDLALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
 Oy 301 FPEKFPFKARDLVKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
 Db 301 FPEKFPFKARDLVKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
 Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQSSGNIQYIHDL 420
 Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQSSGNIQYIHDL 420
 Oy 421 SNSFELDQFSEDEKRLLLSKQAGGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480
 Db 421 SNSFELDQFSEDEKRLLLSKQAGGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480
 Oy 481 GHLYYVDVFNKVLKGIIPWSQLPEAQNPKTFVHTPTARTYLLADPSNAHKMKRQIQ 540
 Db 481 GHLYYVDVFNKVLKGIIPWSQLPEAQNPKTFVHTPTARTYLLADPSNAHKMKRQIQ 540
 Oy 541 EVNRQRYQSHPDAAVQ 556
 Db 541 EVNRQRYQSHPDAAVQ 556

RESULT 2
 Q6FI20_HUMAN

ID Q6FI20_HUMAN PRELIMINARY; PRT; 556 AA.
 AC Q6FI20;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 21-FEB-2006, entry version 10.
 DE PDPK1 protein.
 GN Name=PDPK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Mkoondinya M., Schick M., Eisenstein S.,
 RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LeBeur J.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: CR536517; CAG38755.1; -. mRNA.
 DR SMR: Q6FI20; 72-358, 409-556.
 DR Ensembl: ENSG00000140992; Homo sapiens.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0000166; P:nucleotide binding; IEA.
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011993; PH_type.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 556 AA; 63152 MW; EDBC0306DC4D0653 CRC64;

Oy 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180
 Db 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180
 Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQIOTDPTAKVLSPEKQARAN 240
 Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQIOTDPTAKVLSPEKQARAN 240
 Oy 241 SFVGTAAQVSPPELLTEKSACKSSDLALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
 Db 241 SFVGTAAQVSPPELLTEKSACKSSDLALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300
 Oy 301 FPEKFPFKARDLVKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
 Db 301 FPEKFPFKARDLVKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
 Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQSSGNIQYIHDL 420
 Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQSSGNIQYIHDL 420
 Oy 421 SNSFELDQFSEDEKRLLLSKQAGGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480
 Db 421 SNSFELDQFSEDEKRLLLSKQAGGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480
 Oy 481 GHLYYVDVFNKVLKGIIPWSQLPEAQNPKTFVHTPTARTYLLADPSNAHKMKRQIQ 540
 Db 481 GHLYYVDVFNKVLKGIIPWSQLPEAQNPKTFVHTPTARTYLLADPSNAHKMKRQIQ 540
 Oy 541 EVNRQRYQSHPDAAVQ 556
 Db 541 EVNRQRYQSHPDAAVQ 556

RESULT 3
 ID Q53HJ9_HUMAN PRELIMINARY; PRT; 556 AA.
 AC Q53HJ9;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DR 3-phosphoinositide dependent protein kinase-1 variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 RC MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugeno S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eucaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

Query Match 100.0%; Score 2941; DB 2; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3.5e-184;
 Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGGSROGPAMDGTAAEPRP 60
 Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGGSROGPAMDGTAAEPRP 60
 Oy 61 GAGSLQHAQPPPPQPKRKPDPKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120
 Db 61 GAGSLQHAQPPPPQPKRKPDPKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120

RC TISSUE=Coronary artery;
RX MEDLINE=9803886; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.,
RT "Construction and characterization of a full length-enriched and a 5'-
end-enriched cDNA library";
RL Gene 200:149-156(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Coronary artery;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AK222581; BAD96301.1; -; mRNA.
DR SMR: Q53HJ9; 72-358, 409-556.
DR Ensembl: ENSG00000140992; Homo sapiens.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0000166; P:nucleotide binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 556 AA; 63126 MW; B8ED4F687C7D958C CRC64;

Query Match 99.5%; Score 2926; DB 2; Length 556;
Best Local Similarity 99.5%; Pred. No. 3.4e-183;
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRQTSSTPPGIPGSGRQGPAMDGTAAEPSP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRQTSSTPPGIPGSGRQGPAMDGTAAEPSP 60
Oy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKGRHIK 120
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKGRHIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFVKLYPTFQDDKLYFGLSYAKNGELLYKIRKIGSFDS 180
Db 121 ENKVPYVTRERDVMSRLDHPFVKLYPTFQDDKLYFGLSYAKNGELLYKIRKIGSFDS 180

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
cell stimulation leading to its translocation. Tyrosine
phosphorylation seems to occur only at the plasma membrane (By
similarity).
CC -!- PTM: Phosphorylated on tyrosine and serine/threonine.
CC Phosphorylation on Ser-244 in the activation loop is required for
full activity. PDK1 itself can autophosphorylate Ser-244, leading
to its own activation (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
subfamily.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: Y15748; CAA75758.1; -; mRNA.
DR HSP: Q15530; 1H1W.
DR SMR: Q55173; 75-361, 412-559.
DR Ensembl: ENSRNOG0000006136; Rattus norvegicus.
DR RGD: 620307; Pdk1.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50003; PH_DOMAIN; FALSE_NEG.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 559 3-phosphoinositide-dependent protein
FT kinase 1.
FT FTId=PRO_0000086502.
FT Protein kinase.
FT DOMAIN 85 345 PH.
FT NP_BIND 91 99 ATP (By similarity).
FT COMBIAS 392 399 Poly-Ser.
FT ACT_GITS 208 208 Proton acceptor (By similarity).
FT BINDING 114 114 ATP (By similarity).
FT MOD_RES 9 9 Phosphotyrosine (By similarity).
FT MOD_RES 25 25 Phosphoserine (By similarity).
FT MOD_RES 244 244 Phosphoserine (by autocatalysis) (By
FT similarity).
FT MOD_RES 376 376 Phosphotyrosine (By similarity).
FT MOD_RES 379 379 Phosphotyrosine (By similarity).
FT MOD_RES 396 396 Phosphoserine (By similarity).
FT MOD_RES 399 399 Phosphoserine (By similarity).
FT MOD_RES 406 406 Phosphoserine (By similarity).
FT MOD_RES 413 413 Phosphoserine (By similarity).
SQ SEQUENCE 559 AA; 63609 MW; ADR70A7F6C2A20BF CRC64;

Oy 181 CTRFTTABIIVSALEYLHGKGIHRLDKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFTTABIIVSALEYLHGKGIHRLDKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240
Oy 241 SFVGTAGVYVPELLTEKSACKSSDLWALGCIYQLVAGLPFFRAGNEYLIPQKIILKLYD 300
Db 241 SFVGTAGVYVPELLTEKSACKSSDLWALGCIYQLVAGLPFFRAGNEYLIPQKIILKLYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDAATKRLGCESEMGYGLKAHPFFESVTWENLHQOQPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDAATKRLGCESEMGYGLKAHPFFESVTWENLHQOQPPKLT 360
Oy 361 YLPAMSEDEDEDYGYNDNLSPQGMVSSSSSSSHLSASDTGLPQRSGNIIEQYIHDL 420
Db 361 YLPAMSEDEDEDYGYNDNLSPQGMVSSSSSSSHLSASDTGLPQRSGNIIEQYIHDL 420
Oy 421 SNSFELDLPQSEDEKRLLEKQAGGNPHQFVNNLLQMGVPDKRGLFARRRQLLT 480
Db 421 SNSFELDLPQSEDEKRLLEKQAGGNPHQFVNNLLQMGVPDKRGLFARRRQLLT 480
Oy 481 GPHLYYVDVNVKVLKGSIPWSQLRPAKINFTKFPVHTPNRTYYLMDPSNAHKWCRKI 540
Db 481 GPHLYYVDVNVKVLKGSIPWSQLRPAKINFTKFPVHTPNRTYYLMDPSNAHKWCRKI 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 4
PDPK1_RAT
ID PDPK1_RAT STANDARD; PRT; 559 AA.
AC Q55173;
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (Protein
kinase B kinase) (Pkb kinase).
GN Name=Pdk1; Synonyms=Pdk1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;
RA Stephens L.R., Anderson K.E., Skokos D., Erdjument-Bromage H.,
RA Painter G.P., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,
RA Tempst P., Coadwell W.J., Hawkins P.T.;
RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-
trisphosphate-dependent activation of protein kinase B.";
RL Science 279:710-714(1998).
CC -!- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in
CC signaling processes and in development (By similarity).

Query Match 94.8%; Score 2787.5; DB 1; Length 559;
Best Local Similarity 95.2%; Pred. No. 4.1e-174;
Matches 532; Conservative 6; Mismatches 18; Indels 3; Gaps 2;
Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRQTSSTPPGIPGSGRQGPAMDGTAAEPSP 59
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRQTSSTPPGIPGSGRQGPAMDGTAAEPSP 60
Oy 60 PGAGSLQH--AQQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKGRH 117
Db 61 PSTNLQGHPAQLPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKGRH 120
Oy 118 IIKENKVPYVTRERDVMSRLDHPFVKLYPTFQDDKLYFGLSYAKNGELLYKIRKIGSF 177
Db 121 IIKENKVPYVTRERDVMSRLDHPFVKLYPTFQDDKLYFGLSYAKNGELLYKIRKIGSF 180
Oy 178 DETCTFTTABIIVSALEYLHGKGIHRLDKPENILLNEDMHQIOTDPTAKVLSPEKQAR 237
Db 181 DETCTFTTABIIVSALEYLHGKGIHRLDKPENILLNEDMHQIOTDPTAKVLSPEKQAR 240
Oy 238 RANSFVGTAGVYVPELLTEKSACKSSDLWALGCIYQLVAGLPFFRAGNEYLIPQKIILK 297
Db 241 RANSFVGTAGVYVPELLTEKSACKSSDLWALGCIYQLVAGLPFFRAGNEYLIPQKIILK 300
Oy 298 EYDFPEKFFPKARDLVEKLLVLDAATKRLGCESEMGYGLKAHPFFESVTWENLHQOQPPK 357
Db 301 EYDFPEKFFPKARDLVEKLLVLDAATKRLGCESEMGYGLKAHPFFESVTWENLHQOQPPK 360
Oy 358 LTAYLPAMSEDEDEDYGYNDNLSPQGMVSSSSSSSHLSASDTGLPQRSGNIIEQYIH 417
Db 361 LTAYLPAMSEDEDEDYGYNDNLSPQGMVSSSSSSSHLSASDTGLPQRSGNIIEQYIH 420
Oy 418 DLDNSFELDLPQSEDEKRLLEKQAGGNPHQFVNNLLQMGVPDKRGLFARRRQL 477
Db 421 DLDNSFELDLPQSEDEKRLLEKQAGGNPHQFVNNLLQMGVPDKRGLFARRRQL 480
Oy 478 LTGPHLYYVDVNVKVLKGSIPWSQLRPAKINFTKFPVHTPNRTYYLMDPSNAHKWCR 537
Db 481 LTGPHLYYVDVNVKVLKGSIPWSQLRPAKINFTKFPVHTPNRTYYLMDPSNAHKWCR 540
Oy 538 KIQEVWRQRYQSHPDAAVQ 556
Db 541 KIQEVWRQRYQSHPDAAVQ 559

RESULT 5
PDPK1_MOUSE
ID PDPK1_MOUSE STANDARD; PRT; 559 AA.
AC Q922A0; Q9R1D8; Q9R2L5;
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 18-OCT-2001, sequence version 2.
DT 07-MAR-2006, entry version 44.
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (mPDK1).
GN Name=Pdk1; Synonyms=Pdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver;
RX MBLDINS-99175193; PubMed:10075713; DOI=10.1074/jbc.274.12.8117;
RA Dong L.Q., Zhang R.-B., Langlais P., He H., Clark M., Zhu L., Liu F.;
RT "Primary structure, tissue distribution, and expression of mouse
phosphoinositide-dependent protein kinase-1, a protein kinase that
phosphorylates and activates protein kinase C zeta.";
RL J. Biol. Chem. 274:8117-8122(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RA Park J., Hemmings B.A.;
RT "Mouse phosphoinositide-dependent protein kinase 1 (mPDK1).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C57BL/6;
RA Xu P., Taylor S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in
signaling processes and in development. Could also play a role in
sex differentiation processes.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
cell stimulation leading to its translocation. Tyrosine
phosphorylation seems to occur only at the plasma membrane.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, brain, liver and
testis, also expressed in embryonic cells.
CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.
CC Phosphorylation on Ser-244 in the activation loop is required for
full activity. PDK1 itself can autophosphorylate Ser-244, leading
to its own activation (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF086625; AAC67544.1; -; mRNA.
DR EMBL: AF126294; AAD38505.1; -; mRNA.
DR EMBL: AF079535; AAC96115.1; -; mRNA.
DR HSPB: O15530; 1H1M.
DR SMR: Q922A0; 75-361, 412-559.
DR InAct: Q922A0; -;
DR Ensembl: ENSMUSG00000024122; Mus musculus.
DR MGI: MGI:1338068; Pdk1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. . .; IDA.
DR GO: GO:0006972; P:hyperosmotic response; IDA.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR001849; PH.

DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008371; Ser_thr_kin_AS.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50003; PH_DOMAIN; FALSE_NEG.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;
Serine/threonine-protein kinase; Transferase.
KW CHAIN 1 559 3-phosphoinositide-dependent protein
kinase 1
FT /FTID:PRO_000086501.
FT Protein kinase.
FT DOMAIN 85 345
FT NP_BIND 462 553
FT ACT_SITE 91 99 ATP (By similarity).
FT COMPBIAS 392 401 Poly-Ser.
FT BINDING 208 208 Protein acceptor (By similarity).
FT BINDING 114 114 ATP (By similarity).
FT MOD_RES 9 9 Phosphotyrosine (By similarity).
FT MOD_RES 25 25 Phosphoserine (By similarity).
FT MOD_RES 244 244 Phosphoserine (by autocatalysis) (By
similarity).
FT MOD_RES 376 376 Phosphotyrosine (By similarity).
FT MOD_RES 379 379 Phosphotyrosine (By similarity).
FT MOD_RES 396 396 Phosphoserine (By similarity).
FT MOD_RES 399 399 Phosphoserine (By similarity).
FT MOD_RES 406 406 Phosphoserine (By similarity).
FT MOD_RES 413 413 Phosphoserine (By similarity).
FT CONFLICT 84 84 D -> N (in Ref. 1).
FT CONFLICT 248 248 T -> P (in Ref. 3).
FT CONFLICT 285 285 F -> S (in Ref. 3).
FT CONFLICT 546 546 W -> R (in Ref. 3).
SQ SEQUENCE 559 AA; 63759 MW; 2769.5; DB 1; Length 559;

Query Match 94.24; Score 2769.5; DB 1; Length 559;
Best Local Similarity 94.6%; Pred. No. 6.2e-173;
Matches 529; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

Oy 1 MARTTSQYDAVPIQSSVVLCSPPSMVTRTSSTPPGIPGQ-SROGPAKDQTAEPK 59
Db 1 MARTTSQYDAVPIQSSVVLCSPPSMVTRTSSTPPGIPGQ-SROGPAKDQTAEPK 60
Oy 60 PGAGSLQH-AQPPQPKRKRPRDPKPKGLGSGFSTVVLARSLSREYAIKILKRX 117
Db 61 PSTNPLQHPAQLPQPKRKRPRDPKPKGLGSGFSTVVLARSLSREYAIKILKRX 120
Oy 118 IIKENKVPVYTRERDVMRLHPPFVVLVPTFQDDEKLYFGLSYAKNGELLKYIRKISF 177
Db 121 IIKENKVPVYTRERDVMRLHPPFVVLVPTFQDDEKLYFGLSYAKNGELLKYIRKISF 180
Oy 178 DDTCTRFYTAIVSALSYLHGKGIHRDLKPNILLNEDMHIQITDFQTKVLSPEKQA 237

Db 181 DDTCTRFYTAIVSALSYLHGKGIHRDLKPNILLNEDMHIQITDFQTKVLSPEKQA 240
Oy 238 RANSPVGTAAQYVPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIIL 297
Db 241 RANSPVGTAAQYVPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIIL 300
Oy 298 EYDFPEKFPFKARDLVSKLLVLDATKRLGCSKSGYGLKHPFBSVWNLHQQTTPK 357
Db 301 EYHFPKFPFKARDLVSKLLVLDATKRLGCSKSGYGLKHPFBSVWNLHQQTTPK 360
Oy 358 LTAYLPAMSEDDDCYQNYDNLLSGFGCHVSSSSSSHSLSASDTGLPQSSGSIQYIH 417
Db 361 LTAYLPAMSEDDDCYQNYDNLLSGFGCHVSSSSSSHSLSASDTGLPQSSGSIQYIH 420
Oy 418 DLDSNSFELDQFSEDEKRLLEKAGGNPMHQPVENNLIQMGVVDKRLGFAARRQLL 477
Db 421 DLDTNSFELDQFSEDEKRLLEKAGGNPMHQPVENNLIQMGVVDKRLGFAARRQLL 480
Oy 478 LTGPHLYVYDPNVNKLKGEIPMSQSLRPAKNKTFPVVHTNRTYLYMDPSGNHAKWCR 537
Db 481 LTGPHLYVYDPNVNKLKGEIPMSQSLRPAKNKTFPVVHTNRTYLYMDPSGNHAKWCR 540
Oy 538 KIOEVRWQRYQSHPDAAVQ 556
Db 541 KIOEVRWQRYQSHPDAAVQ 559

RESULT 6
Q3UH20 MOUSE
ID Q3UH20 MOUSE PRELIMINARY; PRT; 559 AA.
AC Q3UH20;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE CDNA, RIKEN full-length enriched library, clone:192018K11 product:3-
DE phosphoinositide dependent protein kinase-1, full insert sequence.
GN Name=Pdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MBLDINS-99279253; PubMed:10349636; DOI=10.1016/S0076-6879(99)03004-3;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aldinis V., Allen J.S.,
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,

Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Putaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojebori T., Green R.S.,
Gustincich S., Harbers M., Hayashizaki Y., Henrich T.K., Hirokawa N.,
Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kato J., Kitamura H.,
Kitano H., Kollmann S.P., Kruger A., Kumerfeldt S.K.,
Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,
Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Moriya K.,
Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekiguchi K., Sempé C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shinada H., Shisada K., Silva D., Sinclair B.,
Sperling S., Stupka K., Sugtara K., Sultana R., Takanaka Y., Taki K.,
Tanno K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen S., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky S., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu S.T., Brusic V., Quackenbush J.,
Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MBLDINS-22354683; PubMed:1246651; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Ose N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojebori T.,
Beldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.S., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kasai A., Kawaji H., Kawasawa Y., Kodzius R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKinnis L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Welle C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Wasth G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayata N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M., Sumi M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL: AK147149; BAB27716.1; -; mRNA.
DR MGI: MGI:1338068; Pdpk1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
DR GO: GO:004676; P:3-phosphoinositide-dependent protein kinase. . .; IDA.
DR GO: GO:0006972; P:hyperosmotic response; IDA.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008371; Ser_thr_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 559 AA; 63729 MW; F0D6AED27161F6B8 CRC64;

Query Match 94.0%; Score 2764.5; DB 2; Length 559;
Best Local Similarity 94.5%; Pred. No. 1,3e-172;
Matches 528; Conservative 8; Mismatches 20; Indels 3; Gaps 2;
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Qy 60 PGAGSLQH--AQPPQPPKPKRPDPFKPKILGEGSPSTVVLARSLSRYAIIKLEKRX 117
Db 61 PSTNPLQHPAQLPQPPKPKRPDPFKPKILGEGSPSTVVLARSLSRYAIIKLEKRX 120
Qy 118 IIKENKVPVYTRERDVMRLDHPFFVLYPTFDDSKLYGLSLYAKNGELLKYIKIGSP 177
Db 121 IIKENKVPVYTRERDVMRLDHPFFVLYPTFDDSKLYGLSLYAKNGELLKYIKIGSP 180
Qy 178 DETCTPTATISVSALEYLHGKGIHRLDKPKNILLNEDMHQITQDFGTAKVLSPEKQA 237
Db 181 DEACTPTATISVSALEYLHGKGIHRLDKPKNILLNEDMHQITQDFGTAKVLSPEKQA 240

Qy 238 RANFVGTAGTQVSPPELLTSKSSDLMALGCIYQLVAGLPFRAGNEYLIFQKIIL 297
Db 241 RANFVGTAGTQVSPPELLTSKSSDLMALGCIYQLVAGLPFRAGNEYLIFQKIIL 300
Qy 298 EYDFPEKFPKARDLVSKLLVDATKGLCEMGYGLKAPHPFSSVTWNLHQOTPPK 357
Db 301 EYDFPEKFPKARDLVSKLLVDATKGLCEMGYGLKAPHPFSSVTWNLHQOTPPK 360
Qy 358 LTAYLPAFSEDDDCYGNYNLLSDFGQVSSSSSSSLASDGLPQRSNNIROYTH 417
Db 361 LTAYLPAFSEDDDCYGNYNLLSDFGQVSSSSSSSLASDGLPQRSNNIROYTH 420
Qy 418 DLOSNSFELDLPSSDESKRLLEKQAQGNPQVFNENLLKMGVDPDKRGLFARRQL 477
Db 421 DLOSNSFELDLPSSDESKRLLEKQAQGNPQVFNENLLKMGVDPDKRGLFARRQL 480
Qy 478 LTBEPHLYVDPVNVKVLKGEIPWSQELRPAKNKFTFVPTNRTTYLMDPSGNAHKWCR 537
Db 481 LTBEPHLYVDPVNVKVLKGEIPWSQELRPAKNKFTFVPTNRTTYLMDPSGNAHKWCR 540
Qy 538 KIQEVNRQYQSHPDAAVQ 556
Db 541 KIQEVNRQYQSHPDAAVQ 559

RESULT 7
QJUGNE_MOUSE
ID QJUGNE_MOUSE PRELIMINARY; PRT; 559 AA.
AC QJUGNE;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE melanocyte cDNA, RIKEN full-length enriched library, clone:G270062J02
DE product:3-phosphoinositide dependent protein kinase-1, full insert
DE sequence.
GN Name=Pdpk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fegiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Putaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gotojori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Henrich T.K., Hirokawa N., Hill D., Hummelnick L., Iacono M., Ikeno K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone P., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky M., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka S., Sugura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamashita H., Zabarovsky S., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Pleasay C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Mikaido I., Oeato N., Saito R., Suzuki M., Yamanaoka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Della E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedziarski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Perles G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringvald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varadero R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Iehli Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217651; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehli Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Waki K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishii K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Iehli Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M.,
 RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AKI47835; BAE28171.1; -; mRNA.
 DR MGI: MGI:1338068; Pdpk1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
 DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. . .; IDA.
 DR GO: GO:0006972; P:hyperosmotic response; IDA.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 559 AA; 63687 MW; 74461D027460FAC6 CRC64;

Query Match 93.8%; Score 2758.5; DB 2; Length 559;
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 Matches 527; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

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 Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRQTQESSTPPGIPGG-SRQGPAMDGTAAEPR 60
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Qy 118 IIKENKVPYVTRERDVMSRLDHPFFVKLYFTFQDEKLYFGLSYAKGELLKIRKIGSF 177
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 Qy 478 LTBEPHLYYDVPNNKVLKGIIPMSQSLRPEAKNFKTFPVHTPRTYITLADPSNAHKMR 537
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RESULT 8
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 ID Q81024_MOUSE PRELIMINARY; PRT; 551 AA.
 AC Q81024;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE PDK1 (Fragment).
 GN Name=Pdpk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ;
 RA Brathwaite M., Waelti P., Schlessinger D., Nagaraja R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----

CC -----
 DR EMBL: AY162410; AA017164.1; -; Genomic DNA.
 DR HSP: Q15530; IHW.
 DR SRR: Q81024; 67-353, 404-551.
 DR Ensembl: ENSMUSG00000024122; Mus musculus.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011993; PH_type.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 551 AA; 62870 MW; ACC31D51439282F4 CRC64;

Query Match 92.9%; Score 2732.5; DB 2; Length 551;
 Best Local Similarity 94.6%; Pred. No. 1.6e-170;
 Matches 521; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

Qy 51 YDAVPIQSSVVLSCSPSPMVRQTQESSTPPGIPGG-SRQGPAMDGTAAEPRPGAGSLQH 67
 Db 1 YDAVPIQSSVVLSCSPSPMVRQTQESSTPPGIPGG-SRQGPAMDGTAAEPRPGAGSLQH 60
 Qy 68 --AQQPPQPKRGRPEDFKFGKILGSGSFSTVVLARSLATSRYAIIKILSKRHIIKKNVP 125
 Db 61 HPAPQLPQPKRGRPEDFKFGKILGSGSFSTVVLARSLATSRYAIIKILSKRHIIKKNVP 120
 Qy 126 YVTRERDVMSRLDHPFFVKLYFTFQDEKLYFGLSYAKGELLKIRKIGSFDTCTRFY 185
 Db 121 YVTRERDVMSRLDHPFFVKLYFTFQDEKLYFGLSYAKGELLKIRKIGSFDTCTRFY 180
 Qy 186 TAVIVSALEYLHGKIIRDLKPENILLNEDMHQIQTDPGTAKVLPSPESKQARNSFVGT 245
 Db 181 TAVIVSALEYLHGKIIRDLKPENILLNEDMHQIQTDPGTAKVLPSPESKQARNSFVGT 240
 Qy 246 AQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPEKF 305
 Db 241 AQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPEKF 300
 Qy 306 FPKARDLVEKLLVLDAKRLGCEMEGYGLKAHPFFSVTWENLHQOTPPKLTAYLPAM 365
 Db 301 FPKARDLVEKLLVLDAKRLGCEMEGYGLKAHPFFSVTWENLHQOTPPKLTAYLPAM 360
 Qy 366 SEDDEDCYGNVDNLLSQFGFMQVSSSSSHSLASDTGLPORGSGNI EQYIHLDSNFS 425
 Db 361 SEDDEDCYGNVDNLLSQFGFMQVSSSSSHSLASDTGLPORGSGNI EQYIHLDSNFS 420

Qy 426 LDLPSESEKRLLEKQAGNPNPHQVFNRLILKNGPVDKRGKLFARRRQLLLTSPHLY 485
Db 421 LDLPSESEKRLLEKQAGNPNPHQVFNRLILKNGPVDKRGKLFARRRQLLLTSPHLY 480
Qy 486 YVDPVNVKLGKIPMSQSLRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCKRIQSVWRQ 545
Db 481 YVDPVNVKLGKIPMSQSLRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCKRIQSVWRQ 540
Qy 546 RYQSHPDAAVQ 556
Db 541 QYQSNPDAAVQ 551

RESULT 9

Q8K3L3_MOUSE
ID Q8K3L3_MOUSE PRELIMINARY; PRT; 532 AA.
AC Q8K3L3;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE Phosphoinositide-dependent protein kinase-1 beta.
GN Name=Pdk1; Synonyms=Pdk1beta;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22050196; PubMed=12054753; DOI=10.1016/S0006-291X(02)00449-7;
RA Dong L.Q., Ramos F.J., Wick M.J., Lim M.A., Guo Z., Strong R.,
RA Richardson A., Liu F.;
RT "Cloning and characterization of a testis and brain-specific isoform
of mouse 3'-phosphoinositide-dependent protein kinase-1, mPDK-1
beta.";
RL Biochem. Biophys. Res. Commun. 294:136-144(2002).
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AY062008; AAL47185.1; -, mRNA.
DR HSSP: O15530; 1H1W.
DR SMR: Q8K3L3; 48-134, 385-532.
DR Ensembl: ENSMUSG0000024122; Mus musculus.
DR WGI: WGI:1338068; Pdk1.
DR GO: GO:0005737; Cytoplasm; IDA.
DR GO: GO:0016023; Cytoplasmic membrane-bound vesicle; IDA.
DR GO: GO:004676; P:3-phosphoinositide-dependent protein kinase. . .; IDA.
DR GO: GO:0006972; P:hyperosmotic response; IDA.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.

DT 15-MAR-2005, sequence version 1.
DT 21-FEB-2006, entry version 10.
DE Hypothetical protein.
GN ORFNames=RCJMB04_6p10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CB; TISSUE=Bursa;
RC Caldwell R.B., Kierzek A.M., Arakawa K., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagoderaki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL: AJ851556; CAH65190.1; -, mRNA.
DR SMR: Q5F3U4; 75-361, 412-555.
DR GO: GO:0005524; P:ATP binding; ISA.
DR GO: GO:000166; P:nucleotide binding; ISA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 556 AA; 63068 MW; 81ED935D6C3E04C9 CRC64;

Query Match 89.3%; Score 2626.5; DB 2; Length 556;
Best Local Similarity 90.5%; Pred. No. 1.5e-163;
Matches 504; Conservative 15; Mismatches 33; Indels 5; Gaps 4;

Qy 1 MASTTSOLYDAVPIQSSVVLCSPPSMVNRQADSTPVSISTQSSGNSMESTAASSR 59
Db 1 MASTSSHLVDAVPIQSSVVLCSPPSMVNRQADSTPVSISTQSSGNSMESTAASSR 59
Qy 60 PGAGSL-QH-AQPPPPQPRKIKRDPDFKPKILGSGSFSTVLARELTSSRYAIKILEKRX 117
Db 61 SSSNSLPQHTGOOPQPRKIKRDPDFKPKILGSGSFSTVLARELTSSRYAIKILEKRX 120

DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 532 AA; 60934 MW; F90731C7ECDE589 CRC64;

Query Match 89.3%; Score 2626.5; DB 2; Length 532;
Best Local Similarity 94.2%; Pred. No. 1.4e-163;
Matches 501; Conservative 9; Mismatches 19; Indels 3; Gaps 2;

Qy 28 MVRTQTESSTPPGIPGG-SRQSPAMDGTAAAPRPGAGSLQH--AQPPPPQPRKIKRDPDFK 84
Db 1 MVRTQTESSTPPGIPGG-SRQSPAMDGTAAAPRPGAGSLQH--AQPPPPQPRKIKRDPDFK 60
Qy 85 GKILGEGSFSTVLARELTSSRYAIKILEKRXIIKENKVPVYTRDRVMSRLHPPFVK 144
Db 61 GKILGEGSFSTVLARELTSSRYAIKILEKRXIIKENKVPVYTRDRVMSRLHPPFVK 120
Qy 145 LYFTFQDEKLYPGLSYAKNGELLKYIRKIGSPDSTCTRPPTASIVSALEYHKGKIIHR 204
Db 121 LYFTFQDEKLYPGLSYAKNGELLKYIRKIGSPDSTCTRPPTASIVSALEYHKGKIIHR 180
Qy 205 DLKPFENILLNEDMHQITDPTAKVLSPEKQARANSFVGTAQTVSPPELLTSSACKSSD 264
Db 181 DLKPFENILLNEDMHQITDPTAKVLSPEKQARANSFVGTAQTVSPPELLTSSACKSSD 240
Qy 265 LNALGCIYQLVAGLPPFRAGNSYLIPOKIIKLEYDPPEKFPFKARDLVEKLLVLDATKR 324
Db 241 LNALGCIYQLVAGLPPFRAGNSYLIPOKIIKLEYDPPEKFPFKARDLVEKLLVLDATKR 300
Qy 325 LQCEMBGYPGLKAHPFFSVSTWNLHQOTPKLTAYLPAKSEDDDCYGNVNLDSQFG 384
Db 301 LQCEMBGYPGLKAHPFFSVSTWNLHQOTPKLTAYLPAKSEDDDCYGNVNLDSQFG 360
Qy 385 CMQVSSSSSHSLASDGLPQSSGSIHQYIHDLNNSFELDQPSDESKRLLEKQAG 444
Db 361 CMQVSSSSSHSLASDGLPQSSGSIHQYIHDLNNSFELDQPSDESKRLLEKQAG 420
Qy 445 GNPHQVFNRLILKNGPVDKRGKLFARRRQLLLTSPHLYYVDPVNVKLGKIPMSQSL 504
Db 421 GNPHQVFNRLILKNGPVDKRGKLFARRRQLLLTSPHLYYVDPVNVKLGKIPMSQSL 480
Qy 505 RPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCKRIQSVWRQRYQSHPDAAVQ 556
Db 481 RPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCKRIQSVWRQRYQSHPDAAVQ 532

RESULT 10

Q5F3U4_CHECK
ID Q5F3U4_CHECK PRELIMINARY; PRT; 556 AA.
AC Q5F3U4;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.

Qy 118 IIKENKVPVYTRDRVMSRLHPPFVKLYFTFQDEKLYPGLSYAKNGELLKYIRKIGSF 177
Db 121 IIKENKVPVYTRDRVMSRLHPPFVKLYFTFQDEKLYPGLSYAKNGELLKYIRKIGSF 180
Qy 178 DETCTRPPTASIVSALEYHKGKIIHRDLKPFENILLNEDMHQITDPTAKVLSPEKQA 237
Db 181 DETCTRPPTASIVSALEYHKGKIIHRDLKPFENILLNEDMHQITDPTAKVLSPEKQA 240
Qy 238 RANSFVOTAQTVSPPELLTSSACKSSDLNALGCIYQLVAGLPPFRAGNSYLIPOKIIKL 297
Db 241 RANSFVOTAQTVSPPELLTSSACKSSDLNALGCIYQLVAGLPPFRAGNSYLIPOKIIKL 300
Qy 298 EYDFPPEKFPFKARDLVEKLLVLDATKRLQCEMBGYPGLKAHPFFSVSTWNLHQOTPK 357
Db 301 EYDFPPEKFPFKARDLVEKLLVLDATKRLQCEMBGYPGLKAHPFFSVSTWNLHQOTPK 360
Qy 358 LTAYLPAKSEDDDCYGNVNLDSQFGCMQVSSSSSHSLASDGLPQSSGSIHQYIH 417
Db 361 LTAYLPAKSEDDDCYGNVNLDSQFGCMQVSSSSSHSLASDGLPQSSGSIHQYIH 420
Qy 418 DLDNSFELDQPSDESKRLLEKQAGGNPHQVFNRLILKNGPVDKRGKLFARRRQLL 477
Db 421 DLDNSFELDQPSDESKRLLEKQAGGNPHQVFNRLILKNGPVDKRGKLFARRRQLL 480
Qy 478 LTEGPHLYYVDPVNVKLGKIPMSQSLRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCK 537
Db 481 LTEGPHLYYVDPVNVKLGKIPMSQSLRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCK 540
Qy 538 KIQSVWRQRYQSHPDAA 554
Db 541 KIQSVWRURY--HQWAA 555

RESULT 11

Q3TRL2_MOUSE
ID Q3TRL2_MOUSE PRELIMINARY; PRT; 522 AA.
AC Q3TRL2;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Adult female vagina cDNA, RIKEN full-length enriched library.
DE clone:9930010N10 product:3-phosphoinositide dependent protein kinase-
DE 1, full insert sequence.
GN Name=Pdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed:16141073; DOI=10.1126/science.11112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilmink L.G., Aldridge V., Allen J.S.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla S., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Putaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Guerinich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,
 Hill D., Huminicki L., Iacono M., Iake K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Taber S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada M., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamanihi H., Zabarovsky S., Zhu S., Zimmer A., Hide W., Bult C.,
 Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niinomiya N.,
 Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed:16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE:22354683; PubMed:12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Ikehata I., Ootani N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE:2053083; PubMed:11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,
 Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC
 DR EMBL: AK126777; BAS7017.1; -; mRNA.
 DR MGI: MGI:1338068; Pdpk1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
 DR GO: GO:004676; F:3-phosphoinositide-dependent protein kinase. .; IDA.
 DR GO: GO:0006972; P:hyperosmotic response; IDA.
 DR GO: GO:0007167; P:signal transduction; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_pkin_AS.
 DR InterPro: IPR002290; Ser_Thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DMP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 DR Serine/threonine-protein kinase; Transferase.
 GO SEQUENCE 522 AA; 59328 MW; 4C31B7D53F6306BF CRC64;

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,
 Blake J.A., Brada D., Brusic V., Chothia C., Corbani L.S., Cousins S.,
 Dalla E., Dregani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Guinichich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedziera R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilmink L.G., Wyszynski-Boris A., Yanagisawa M., Yang L., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sasaki D., Shibata K., Shingawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE:21085660; PubMed:11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kushi P., Lewis S., Matsumoto Y., Hakeda I., Pesole G., Quackenbush J.,
 Schriml L.M., Staudt P., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Guinichich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts A.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmink L.,
 Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohda S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE:20499374; PubMed:11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 QY 1 MARTTSQLYDAVPIQSSVVLCSFSPSMVIRTQTSSTPPGIPGG-SROGPMXDTAAEP 59
 DB 1 MARTTSQLYDAVPIQSSVVLCSFSPSMVIRTQTSSTPPGIPGG-SROGPMXDTAAEP 60
 QY 60 PGAGSLQH--AQPPPPK 117
 DB 61 PSTNLQHQHQAQPLQPPK 120
 QY 118 IIKENKVPVYTRDVMKSLDHPFFVLYYFTQDDSKLYPGLSVAKNGLLYIKRIGSF 177
 DB 119 IIKENKVPVYTRDVMKSLDHPFFVLYYFTQDDSKLYPGLSVAKNGLLYIKRIGSF 180
 QY 178 DRTCTRTYATISVSALEYLHKGIIIRDLKPKPNTLLNWDHGIQITDPTAKVLPSPKQA 237
 DB 181 DRTCTRTYATISVSALEYLHKGIIIRDLKPKPNTLLNWDHGIQITDPTAKVLPSPKQA 240
 QY 238 RANSFVGTAQYVSPKLLTEKSAKSSDLWALGCIYIYQVAGLPPFRAGNSYILFQKIKL 297
 DB 241 RANSFVGTAQYVSPKLLTEKSAKSSDLWALGCIYIYQVAGLPPFRAGNSYILFQKIKL 300
 QY 298 EYDFPEKFPFKARDLVKLLVLDATKRLGCEMEGYPGLKAIHPFFSTWENLHQTPPK 357
 DB 301 SYHFPKFPFKARDLVKLLVLDATKRLGCEMEGYPGLKAIHPFFSTWENLHQTPPK 360
 QY 358 LTAYLPAMSEDDDCYGNYNLLSOPGCMQVSSSSSSSHLSASDTLPQRSGNSIYQYIH 417
 DB 361 LTAYLPAMSEDDDCYGNYNLLSOPGCMQVSSSSSSSHLSASDTLPQRSGNSIYQYIH 420
 QY 418 DLDSNSFLDLQPSKSLKLLLEKQAGGNPMQPVNENLILQMPVDKRLPARRRQLL 477
 DB 421 DLDTNSFLDLQPSKSLKLLLEKQAGGNPMQPVNENLILQMPVDKRLPARRRQLL 480
 QY 478 LTRGPHLYYDVPNKVLEKSIIPWSQELRPAKNGKTPFVHT 518
 DB 481 LTRGPHLYYDVPNKVLEKSIIPWSQELRPAKNGKTPFVHT 521
 RESULT 12
 ID Q5480_TETNG
 AC Q5480 PRELIMINARY; PRT; 558 AA.
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 GN Chromosome 2 SCAP14738, whole genome shotgun sequence. (Fragment).
 ORFNames=GSTENG00024075001;
 OS Tetradon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 Mauviel S., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Query Match 87.1%; Score 2560.5; DB 2; Length 522;
 Best Local Similarity 94.6%; Pred. No. 2.8e-159;
 Matches 493; Conservative 6; Mismatches 19; Indels 3; Gaps 2;

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desilve C., Salenbaum M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Rubin C., Castellani V., Kacinski M., Vacherie S.,
RA Biemont C., Skalli Z., Cattolico L., Poulsen J., De Berardinis V.,
RA Cruaud C., Duprat S., Brothier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudat V., Schachter V., Quetier F., Saurin M., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RM (2)
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC respective C-terminus of RNA polymerase II. Catalytic component of
CC MPF (by similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (by similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CAAG01014738; CAG04372.1; -, Genomic DNA.
DR SMR; Q45480; 78-364, 417-557.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000166; P:nucleotide binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD0000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 558 558
SQ SEQUENCE 558 AA; 63806 MW; 4E0997DA7344C73A CRC64;

Query Match 81.3%; Score 2391.5; DB 2; Length 558;
Best Local Similarity 81.7%; Pred. No. 3.7e-148;
Matches 455; Conservative 43; Mismatches 52; Indels 7; Gaps 4;

Oy 1 MARTTSQLYDAVPIQSSVVLCSCTSPSMVTRTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 59
Db 1 MARATSQLYDVVPIQSSVVLCSCTSPSMVTRTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 60

Oy 60 ----PGAGSLQHAQPP-PPRKRKPEDPKFGKILGSGSPSTVVLARELATSREYAIKILK 114
Db 61 LDGASGSGTQAARPPQPKPKKQSPDPKFGKILGSGSPSTVVLARELATSREYAIKILK 120

Oy 115 KRHIKENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYPGLSYAKGSKLLKYIRKI 174
Db 121 KRHIKENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYPGLSYAKGSKLLKYIRKI 180

Oy 175 GSPDFTCTRPYTAIVSALYLGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPE 234
Db 181 GSPDFTCTRPYTAIVSALYLGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPE 240

Oy 235 KOARANSFVGTQAVSPPELLTEKSACKSDLMALGCIYQVLVAGLPPFRAGNEYLIPOKI 294
Db 241 KOARANSFVGTQAVSPPELLTEKSACKSDLMALGCIYQVLVAGLPPFRAGNEYLIPOKI 300

Oy 295 IKLEYDFPEKFPFKARDLVEKLLVLDATKRLGCEMEGYGPKAHPFFSVTWNHQQTPPKLTA 354
Db 301 IKLEYDFPEKFPFKARDLVEKLLVLDATKRLGCEMEGYGPKAHPFFSVTWNHQQTPPKLTA 360

Oy 355 PKLTAYLPAWSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQSGSNIE 413
Db 361 PKLTAYLPAWSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQSGSNIE 420

Oy 414 QYIHDLNNSFELDLPQSSSEKRLLEKQAGNPMHGFVFNENILJMGVPDKRGLFARR 473
Db 421 QYIHDLNNSFELDLPQSSSEKRLLEKQAGNPMHGFVFNENILJMGVPDKRGLFARR 480

Oy 474 ROLLTTEPHLYVYDPPVNVKLGKIPMSQELRPEAKNFKTPFVHTPNRTTYLMDPSGNH 533
Db 481 ROLLTTEPHLYVYDPPVNVKLGKIPMSQELRPEAKNFKTPFVHTPNRTTYLMDPSGNH 540

Oy 534 KNCRKIQSVWRQYQSH 550
Db 541 KNCRKIQSVWRQYQSH 557

RESULT 13
Q59EH6 HUMAN
ID Q59EH6 HUMAN PRELIMINARY; PRT; 492 AA.
AC Q59EH6;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 3-phosphoinositide dependent protein kinase-1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB209835; BAD93072.1; -, mRNA.
DR SMR; Q59EH6; 110-396.
DR Ensembl; ENSG00000140992; Homo sapiens.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000166; P:nucleotide binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000169; Pept_cys_AS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 492 AA; 54828 MW; A8BA2A6F7C98E26 CRC64;

Query Match 79.4%; Score 2336; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSCTSPSMVTRTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 60
Db 39 MARTTSQLYDAVPIQSSVVLCSCTSPSMVTRTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 98

Oy 61 GAGSLQHAQPPQPKRKRPEPKFGKILGSGSPSTVVLARELATSREYAIKILKSKHIIK 120
Db 99 GAGSLQHAQPPQPKRKRPEPKFGKILGSGSPSTVVLARELATSREYAIKILKSKHIIK 158

Oy 121 ENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYPGLSYAKGSKLLKYIRKISGPDST 180
Db 159 ENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYPGLSYAKGSKLLKYIRKISGPDST 218

Oy 181 CTRPYTAIVSALYLGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 219 CTRPYTAIVSALYLGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 278

Oy 241 SPVGTQAVSPPELLTEKSACKSDLMALGCIYQVLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 279 SPVGTQAVSPPELLTEKSACKSDLMALGCIYQVLVAGLPPFRAGNEYLIPOKIKLEYD 338

Oy 301 FPEKFPFKARDLVEKLLVLDATKRLGCEMEGYGPKAHPFFSVTWNHQQTPPKLTA 360
Db 339 FPEKFPFKARDLVEKLLVLDATKRLGCEMEGYGPKAHPFFSVTWNHQQTPPKLTA 398

Oy 361 YLPAMSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQSGSNIEQYIHDL 420
Db 399 YLPAMSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQSGSNIEQYIHDL 458

Oy 421 SNSFELDLPQSSSEKRLLEKQAGNPM 447
Db 459 SNSFELDLPQSSSEKRLLEKQAGNPM 485

RESULT 14
Q6NZV1 BRARE
ID Q6NZV1 BRARE PRELIMINARY; PRT; 537 AA.
AC Q6NZV1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Hypothetical protein zgc:77318.
GN ORFNames=zgc:77318;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.O., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Viallon D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green S.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smaluk D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

Qy	1	MARTTSQLYDAVPIQSSVVLGSCSPSMVTRTETSSTPGIPGSGRGQPMADQTAASPRP	60
Db	1	MARATSQIYDAVSLSS-VLISC-PSMVRGQDT-----PRHGNSSMEGPA-----P	45
Qy	61	GAGSLQHAQPPPOPKRKPEDFKPGKILGEGSFSTVVLARELSATSEYAIKILSRHIK	120
Db	46	NA-----QPAQPKRPPRDPFRGKILGEGSFSTVVLAKHTTGKGYAIKILSRHIK	98
Qy	121	ENKVPYVTRERDVRSLRPLPVLTPQDQSLKAGKAGKLLKYIKIGSFDST	180
Qy	99	ENKAQYVKRERDISHLHNPFFVLYVTPQDSKLYGLSYAKGSKLLKYIKIGSFDST	158
Qy	181	CTRPYTAIEISALSYLHGKI IHRDLKPENI LLNEEMHGIITDPGTAKLSSPSQKARN	240
Qy	159	CTRPYSAIEI CALEYLHGKI IHRDLKPENI LLSEEMHGIITDPGTAKLSSDSQKARN	218
Qy	241	SPVGTAAQYVSPELLTEKSACKSSDLNAGLCI IYLVAGLPPFRAGNEYLIKQIKLEYD	300
Db	219	SPVGTAAQYVSPELLTEKSACKSSDLNAGLCI IYLVAGLPPFRAGNEYLIKQIKLEYE	278
Qy	301	PFKFFPKIARDVEKLLVLDAITKRLCEDEMGYGPILKHPFFSVETWNIHQQTPPILTA	360

[illegible]

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RESULT 15
Q9BRD5_HUMAN
ID Q9BRD5_HUMAN PRELIMINARY; PRT; 429 AA.
OC Q9BRD5; Q8IV52;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, sequence version 2.
DT 07-FEB-2006, entry version 29.
DE 3-phosphoinositide dependent protein kinase-1 (PDPK1 protein).
GN Name=PDPK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Uterus;
RX MEDLINE=323388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavent T.L., Scheetz T.S.,
RA Brownstein M.J., Ustin T.B., Tsohylyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Gordergen E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shvechenko Y., Bouffard G.G.,
RA Blakeau R.M., Touchan J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalka U., Smalls D.E.,
RA Schnercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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Search completed: June 27, 2006, 01:36:19
Job time : 302 secs

Search completed: June 27, 2006, 01:36:19
Job time : 302 secs

OM protein - protein search, using sw model

Run on: June 26, 2006, 23:38:12 ; Search time 196 Seconds
(without alignments)
1297.002 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPVQSSVVL.....RKIGSVWRQRYQSHPDAAVQ 556

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseq1980a:*
2: geneseq1990a:*
3: geneseq2000a:*
4: geneseq2001a:*
5: geneseq2002a:*
6: geneseq2003a:*
7: geneseq2003ba:*
8: geneseq2004a:*
9: geneseq2005a:*
10: geneseq2006a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2941	100.0	556	2 AAW71738	Aaw71738 Human 3-p
2	2941	100.0	556	2 AAY27055	Aay27055 Human pro
3	2941	100.0	556	3 AAB28445	Aab28445 Human PDK
4	2941	100.0	556	3 AAB28446	Aab28446 Human PDK
5	2941	100.0	556	3 AAY94735	Aay94735 Phosphoin
6	2941	100.0	556	6 ABO07176	Ab007176 Human p53
7	2941	100.0	556	6 ABU04708	Abu04708 Human exp

XX
PN W09841638-A1.
XX
PD 24-SEP-1998.
XX
PF 16-MAR-1998; 98WO-GB000777.
XX
PR 17-MAR-1997; 97GB-00005462.
PR 19-JUN-1997; 97GB-00012826.
PR 15-AUG-1997; 97GB-00017253.
PR 03-OCT-1997; 97US-00943667.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Alessi DR;
XX
DR WPI; 1998-531572/45.
DR N-PSDB; AAV61037.
XX
PT New isolated 3-phosphoinositide-dependent protein kinase - which
PT phosphorylates and activates protein kinase B-alpha, used to develop
PT products for treating diabetes or cancers or for enhancing cell
PT proliferation.
XX
PS Example 2; Fig 10; 120pp; English.
XX
CC A pure 3-phosphoinositide-dependent protein kinase (3PDPK) that
CC phosphorylates and activates PK B-alpha has been isolated. The present
CC sequence represents human 3PDPK. Products from the present invention
CC (e.g. 3PDPK, nucleotide sequence encoding 3PDPK, antibodies against
CC 3PDPK) can be used to identify compounds which modulate the PK activity
CC e.g. for treating diabetes or cancers or for enhancing cell proliferation
CC in the regeneration of nerves or in wound healing
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPVQSSVVLCSPPSMVTRTSTSTPPGPGGSRQGPAMDQAAEPRP 60
Db 1 MARTTSQLYDAVPVQSSVVLCSPPSMVTRTSTSTPPGPGGSRQGPAMDQAAEPRP 60
Oy 61 GAGSLQHAQPPQPRQPRDFKPGKILGEGSPSTVVLARELATSTREYA1KILKRIIHK 120
Db 61 GAGSLQHAQPPQPRQPRDFKPGKILGEGSPSTVVLARELATSTREYA1KILKRIIHK 120
Oy 121 ENKVPVYTRERDVRSLDHPFFVKLYPTQDDKLYFGLSYAOKGELLKYIRKIGSFDET 180
Db 121 ENKVPVYTRERDVRSLDHPFFVKLYPTQDDKLYFGLSYAOKGELLKYIRKIGSFDET 180
Oy 181 CTRPYTARIVSALEYLHGKQIIRDLKPENILLNEDMHIQITDGTAKVLSPPSKQARAN 240
Db 181 CTRPYTARIVSALEYLHGKQIIRDLKPENILLNEDMHIQITDGTAKVLSPPSKQARAN 240
Oy 241 SPVGTAAQYVSPPELLTEKSAKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKI1KLEBYD 300

8	2941	100.0	556	6 ABU04718	Abu04718 Human exp
9	2941	100.0	556	6 ABU04712	Abu04712 Human exp
10	2941	100.0	556	6 ABU04716	Abu04716 Human exp
11	2941	100.0	556	6 ABU04711	Abu04711 Human exp
12	2941	100.0	556	6 ABU04706	Abu04706 Human exp
13	2941	100.0	556	6 ABU04714	Abu04714 Human exp
14	2941	100.0	556	6 ABU04707	Abu04707 Human exp
15	2941	100.0	556	6 ABU04717	Abu04717 Human exp
16	2941	100.0	556	7 ABM79012	Abm79012 Human pho
17	2941	100.0	556	7 ADD44919	Add44919 Human Pro
18	2941	100.0	556	7 ADD44915	Add44915 Human Pro
19	2941	100.0	556	7 ADD89983	Add89983 Human can
20	2941	100.0	556	8 ADI36055	Adi36055 Human pho
21	2941	100.0	556	8 ADI36055	Adi36055 Human PDP
22	2941	100.0	556	8 ADQ19234	Adq19234 Human eof
23	2937	99.9	556	2 AAY05779	Aay05779 Human pro
24	2889.5	98.2	599	8 ABM84519	Abm84519 Human dia
25	2838	96.5	535	4 AAB99823	Aab99823 AGC prote
26	2838	96.5	535	6 ABU04713	Abu04713 Human exp
27	2787.5	94.8	559	7 ADD44917	Add44917 Rat Prote
28	2787.5	94.8	559	7 ADD44913	Add44913 Rat Prote
29	2682	91.2	506	2 AAY05780	Aay05780 Human pro
30	2682	91.2	506	6 ABU04715	Abu04715 Human exp
31	2360	80.2	462	10 AEF60044	Aef60044 Human tru
32	2202.5	74.9	468	6 ABU04719	Abu04719 Human exp
33	2202.5	74.9	468	6 ABU04705	Abu04705 Human exp
34	1893	64.4	361	9 ADY85535	Ady85535 Catalytic
35	1747	59.4	335	4 AAB99847	Aab99847 AGC prote
36	1747	59.4	335	8 ADJ38895	Adj38895 PDK1 amin
37	1710	58.1	319	6 ABU04709	Abu04709 Human exp
38	1710	58.1	319	6 ABU04720	Abu04720 Human exp
39	1513	51.4	289	8 ADJ38865	Adj38865 PDK1 amin
40	1486	50.5	285	6 ABR57461	Abr57461 AGC famil
41	1144.5	38.9	752	4 ABB57927	Abb57927 Drosophil
42	1144.5	38.9	752	4 ABB67127	Abb67127 Drosophil
43	1144.5	38.9	752	4 ABB57782	Abb57782 Drosophil
44	1144.5	38.9	752	4 ABB67126	Abb67126 Drosophil
45	973	33.1	539	4 ABB67129	Abb67129 Drosophil

ALIGNMENTS

RESULT 1

AAW71738
ID AAW71738 standard; protein; 556 AA.
XX
AC AAW71738;
XX
DT 10-DEC-1998 (first entry)
XX
DE Human 3-phosphoinositide-dependent protein kinase.
XX
KW Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;
KW diabetes; cancer; cell proliferation; phosphorylation.
XX
OS Homo sapiens.

Db 241 SPVGTAAQYVSPPELLTEKSAKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKI1KLEBYD 300
Oy 301 FFSKFFPKARDLVSKLLVLVDATKRLGCSMEGYGLKAHPFFSVTWENLHQOTPPKLT 360
Db 301 FFSKFFPKARDLVSKLLVLVDATKRLGCSMEGYGLKAHPFFSVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDCYGNVDNLISQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDDCYGNVDNLISQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Oy 421 SNSFELDQLQFSEDEKRLLEKQAGGNPMHQFVENNLI1KMGVPDKRGLPARRRQLLITE 480
Db 421 SNSFELDQLQFSEDEKRLLEKQAGGNPMHQFVENNLI1KMGVPDKRGLPARRRQLLITE 480
Oy 481 GHLYYVDVPMKVLKGSIPWSQELRPAENKFTFPVHTPNRTTYLMDPSGNAHMKCRKI 540
Db 481 GHLYYVDVPMKVLKGSIPWSQELRPAENKFTFPVHTPNRTTYLMDPSGNAHMKCRKI 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 2

AAV27055
ID AAY27055 standard; protein; 556 AA.
XX
AC AAY27055;
XX
DT 08-OCT-1999 (first entry)
XX
DE Human protein kinase (HPKM)-4 (clone ID 472480).
XX
KW Human protein kinase molecule; HPKM; human; protein kinase;
KW phosphate group; cancer; immune disorder.
XX
OS Homo sapiens.
XX
PN W09931981-A2.
XX
PD 05-AUG-1999.
XX
PF 12-JAN-1999; 99WO-US000661.
XX
PR 30-JAN-1998; 98US-00016000.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Hillman JL, Lal P, Akerblom IS, Shah P, Corley NC;
PI Ouegler KJ;
XX
DR WPI; 1999-479190/40.
DR N-PSDB; AAX89853.
XX
PT New human protein kinase molecules useful for treating or preventing
PT cancer or an immune disorder.

XX
PS Claim 1; Page 68-69; 77pp; English.
XX
CC The invention provides human protein kinase molecules (HPKM) (AAY27052-
CC 57) and nucleic acid sequences (AAX89850-55) encoding the HPKM
CC polypeptides respectively. The HPKM polypeptides can be produced
CC recombinantly by standard recombinant methodology. Protein kinases add
CC phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is
CC used to treat or prevent cancer or an immune disorder. The present
CC sequence represents the amino acid sequence of HPKM-4
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Oy 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Db 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Oy 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Oy 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Db 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Db 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Oy 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Db 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Oy 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Oy 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Db 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Db 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 4
AAB28446
ID AAB28446 standard; protein; 556 AA.
XX
AC AAB28446;
XX
DT 01-FEB-2001 (first entry)
XX
DS Human PDK-1.
XX
KW Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;
KW antisense oligonucleotide; phosphorothioate; antiinflammatory;
KW cytostatic; antimicrobial.
XX
OS Homo sapiens.
XX
PN US6124272-A.

RESULT 3
AAB28445
ID AAB28445 standard; protein; 556 AA.
XX
AC AAB28445;
XX
DT 01-FEB-2001 (first entry)
XX
DS Human PDK-1.
XX
KW Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;
KW antisense oligonucleotide; phosphorothioate; antiinflammatory;
KW cytostatic; antimicrobial.
XX
OS Homo sapiens.
XX
PN US6124272-A.
XX
PD 26-SEP-2000.
XX
PF 09-APR-1999; 99US-00289466.
XX
PR 09-APR-1999; 99US-00289466.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowseert LM;
XX
DR WPI; 2000-611015/58.
DR N-PSDB; AAC60590.
XX

PT Novel antisense compounds useful for inhibiting the expression of human 3
PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating
PT inflammation, tumors and infections.
XX
PS Disclosure; Col 45-48; 41pp; English.
XX
CC The nucleotide sequence encoding the present protein was used to design a
CC large number of antisense oligonucleotides which are targeted to a
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or
CC chimeric oligonucleotides containing a central gap region, consisting of
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate
CC backbone. The antisense oligonucleotides are useful for inhibiting the
CC expression of human PDK-1 in human cells or tissues. They are also useful
CC for preventing or delaying infection, inflammation or tumors and are
CC useful for research and diagnostics
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Oy 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Db 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Oy 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Oy 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Db 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLKHPPFESSVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Db 361 YLPAMSEDDDEDYGNYNLLSQFGCMQVSSSSSHSLASDTGLPQRSGSNI EGYIHDL 420
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPWQVNNLILKMGVVDKRGKLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Db 481 GPHLYYVDPVNKLKGI PWSQSLRPAKQNFKTFPVHTPNRTTYLMDPSGNAHWCKRKIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

XX
PD 26-SEP-2000.
XX
PF 09-APR-1999; 99US-00289466.
XX
PR 09-APR-1999; 99US-00289466.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowseert LM;
XX
DR WPI; 2000-611015/58.
DR N-PSDB; AAC60591.
XX
PT Novel antisense compounds useful for inhibiting the expression of human 3
PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating
PT inflammation, tumors and infections.
XX
PS Disclosure; Col 49-52; 41pp; English.
XX
CC The nucleotide sequence encoding the present protein was used to design a
CC large number of antisense oligonucleotides which are targeted to a
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or
CC chimeric oligonucleotides containing a central gap region, consisting of
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate
CC backbone. The antisense oligonucleotides are useful for inhibiting the
CC expression of human PDK-1 in human cells or tissues. They are also useful
CC for preventing or delaying infection, inflammation or tumors and are
CC useful for research and diagnostics
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60
Oy 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Db 61 GAGSLQHAQPPPPQPRKGRPEDPKFKILGSGFSTVVLARELATSREYA IKILSKRHIIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Oy 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGI IHRDLKPENILNEDMHQIOTDPTAKVLSPEKQARAN 240
Oy 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300
Db 241 SFVOTAQYVSPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI IKLEYD 300

Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNVNLISQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDL 420
Db 361 YLPAMSEDDSDCYGNVNLISQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDL 420
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHOFVENNLILKMGVDPDKRGLFARRRQLL 480
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHOFVENNLILKMGVDPDKRGLFARRRQLL 480
Qy 481 GPHLYYVDPVNVKLGSIWMSQLRPAKQKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNVKLGSIWMSQLRPAKQKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 5

AAI94735
ID AAI94735 standard; protein; 556 AA.
XX
AC AAI94735;
XX
DT 29-JAN-2001 (first entry)
XX
DE Phosphoinositide dependent protein kinase 1 (PKD1).
XX
KW Substrate specificity; phosphoinositide-dependent protein kinase 1; PKD1;
KW protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
KW mechanical tissue damage; ischaemic disease; stroke;
KW myocardial infarction; antigenic peptide.
XX
OS Unidentified.
XX
PN WO200056864-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB001004.
XX
PR 19-MAR-1999; 99GB-0006245.
XX
PA (UYDU-) UNIV DUNDSE.
XX
PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
XX
DR WPI; 2000-647155/62.
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
PT interacting polypeptide.
XX

Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNVNLISQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDL 420
Db 361 YLPAMSEDDSDCYGNVNLISQPGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDL 420
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHOFVENNLILKMGVDPDKRGLFARRRQLL 480
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHOFVENNLILKMGVDPDKRGLFARRRQLL 480
Qy 481 GPHLYYVDPVNVKLGSIWMSQLRPAKQKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNVKLGSIWMSQLRPAKQKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 6

ABO07176
ID ABO07176 standard; protein; 556 AA.
XX
AC ABO07176;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human p53 modifying protein, SEQ ID 136.
XX
KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
KW apoptotic disorder; cell proliferation disorder.
XX
OS Homo sapiens.
XX
PN WO200399122-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017382.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Punke RP;
XX
DR WPI; 2003-156859/15.
DR N-PSDB; ACD13352.
XX
PT Identifying modulators of the p53 pathway for use in treating apoptotic
PT or cell proliferation disorders, comprises screening for agents that

PS Disclosure; Fig 10; 103pp; English.

XX
CC This invention relates to a method for altering the substrate specificity
CC of phosphoinositide-dependent protein kinase 1 (PKD1), by exposing it to
CC an interacting polypeptide. Included in the invention are a preparation
CC comprising PKD1 and an interacting polypeptide, PKD1 with altered
CC specificity is useful for phosphorylating a residue corresponding to the
CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
CC -Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PKD1 is also used for phosphorylating
CC protein kinase C related protein kinase 2 (PRK2). The compound identified
CC by methods of the invention that are capable of altering the substrate
CC specificity of PKD1 are useful for manufacturing a medicament for
CC treating a patient who is in need of modulation of the insulin signalling
CC pathway and/or PKD1, PKD2 or PRK2 signalling. A compound that is capable
CC of reducing the activity (i.e. the PKD1 and/or the PKD2 activity) of PKD1
CC may be useful in treating cancer. PKD1, e.g. via protein kinase B and/or
CC SGK, may be capable of providing a survival signal that protects cells
CC from apoptosis induced in a variety of ways. Reduction of the activity of
CC PKD1 may promote apoptosis and may be useful in treating cancer.
CC Conditions in which aiding apoptosis may be benefit may also include
CC resolution of inflammation. A compound capable of increasing the activity
CC of PKD1 may be useful in treating diabetes or obesity, or may be useful
CC in inhibiting apoptosis. Increased activity of PKD1 may lead to increased
CC levels of leptin, which may lead to weight loss. The compounds may
CC suppress apoptosis, which may aid cell survival during or following cell
CC damaging processes and in treating disease in which apoptosis is
CC involved. Examples of the diseases include, mechanical (including heat)
CC tissue injury or ischaemic disease, for example stroke and myocardial
CC infarction, or neural injury. The present sequence represents a
XX phosphoinositide-dependent-protein kinase 1 amino acid sequence
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVOTESTTTPGIPGSGRQGPAMQGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVOTESTTTPGIPGSGRQGPAMQGTAAEPRP 60
Qy 61 GAGSLQHAQPPPPQPKRKPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRII 120
Db 61 GAGSLQHAQPPPPQPKRKPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRII 120
Qy 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYLPGSLYAKNGELLYIKIKIGSFDET 180
Db 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYLPGSLYAKNGELLYIKIKIGSFDET 180
Qy 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILNEDMHQITDPTGAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILNEDMHQITDPTGAKVLSPEKQARAN 240
Qy 241 SFVGTAYQVSPPELLTSACKSSDGLWALGCIYQLVAGLPPFRAGNEYLIKIFOKIKLEYD 300
Db 241 SFVGTAYQVSPPELLTSACKSSDGLWALGCIYQLVAGLPPFRAGNEYLIKIFOKIKLEYD 300

PT modulate activity of a human ortholog of genes that modify the p53
PT pathway in Drosophila.
XX

PS Example 2; Page 439-440; 678pp; English.

XX
CC The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising
CC contacting a cell defective in p53 function with a candidate modulator
CC that specifically binds to a HM polypeptide comprising an HM amino acid
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
CC in a mammalian cell (comprising contacting the cell with an agent that
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
CC a disease in a patient (comprising: (a) obtaining a biological sample
CC from the patient; (b) contacting the sample with a probe for HM
CC expression; (c) comparing the results with a control; and (d) determining
CC whether the comparison indicates a likelihood disease). (M1) is useful
CC for identifying modulators of the p53 pathway. A probe for HM expression
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
CC in a patient, where the cancer has greater than 25 % expression level.
CC Modulators identified by (M1) are useful in a variety of diagnostic and
CC therapeutic applications, where disease or disorder prognosis is related
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
CC the p53 function of the cell, so that the cell undergoes normal
CC proliferation or progression through the cell cycle. (M2) and (M3) are
CC also useful for treating defects in the p53 pathway such as angiogenic,
CC apoptotic or cell proliferation disorders. The present sequence
XX represents a human p53 pathway modifying protein
XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVOTESTTTPGIPGSGRQGPAMQGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVOTESTTTPGIPGSGRQGPAMQGTAAEPRP 60
Qy 61 GAGSLQHAQPPPPQPKRKPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRII 120
Db 61 GAGSLQHAQPPPPQPKRKPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRII 120
Qy 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYLPGSLYAKNGELLYIKIKIGSFDET 180
Db 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYLPGSLYAKNGELLYIKIKIGSFDET 180
Qy 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILNEDMHQITDPTGAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILNEDMHQITDPTGAKVLSPEKQARAN 240

Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
Oy 361 YLPAMSEDDSDCYGNYDNLSSQFGCMQVSSSSSSSHLSASDTGLPQRSQSGNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYDNLSSQFGCMQVSSSSSSSHLSASDTGLPQRSQSGNIQYIHDLD 420
Oy 421 SNSFELDLPQSEDSKRLLEKQAGGNPMHQFVNNLILKMGVPDKRGLFARRRQLLLTE 480
Db 421 SNSFELDLPQSEDSKRLLEKQAGGNPMHQFVNNLILKMGVPDKRGLFARRRQLLLTE 480
Oy 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Db 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 7

ABU04708
ID ABU04708 standard; protein; 556 AA.
XX
AC ABU04708;
XX
DT 29-JAN-2003 (first entry)
XX
DS Human expressed protein tag (EPT) #1374.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.

RESULT 8

ABU04718
ID ABU04718 standard; protein; 556 AA.
XX
AC ABU04718;
XX
DT 29-JAN-2003 (first entry)
XX
DS Human expressed protein tag (EPT) #1384.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX

XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1374; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60
Oy 61 GAGSLQAQPPPPQPKRGPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIYK 120
Db 61 GAGSLQAQPPPPQPKRGPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIYK 120
Oy 121 ENKVPYVTRERDVMKRLDHPFFVKLYPTFQDDSKLYFGLSYAOKGELLKYIRKISFDST 180
Db 121 ENKVPYVTRERDVMKRLDHPFFVKLYPTFQDDSKLYFGLSYAOKGELLKYIRKISFDST 180
Oy 181 CTRFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1384; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60
Oy 61 GAGSLQAQPPPPQPKRGPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIYK 120
Db 61 GAGSLQAQPPPPQPKRGPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIYK 120
Oy 121 ENKVPYVTRERDVMKRLDHPFFVKLYPTFQDDSKLYFGLSYAOKGELLKYIRKISFDST 180
Db 121 ENKVPYVTRERDVMKRLDHPFFVKLYPTFQDDSKLYFGLSYAOKGELLKYIRKISFDST 180
Oy 181 CTRFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Oy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQOTPPKILTA 360
Oy 361 YLPAMSEDDSDCYGNYDNLSSQFGCMQVSSSSSSSHLSASDTGLPQRSQSGNIQYIHDLD 420

Db 361 YLPAMSEDDSDCYGNYDNLSSQPGCMQVSSSSSSSLASDGLPQRSGSNIEQYIHDLQ 420
Oy 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480
Oy 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Db 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 9

ABU04712
ID ABU04712 standard; protein; 556 AA.
XX
AC ABU04712;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (SPT) #1378.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX

Oy 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Db 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Oy 541 EVMRQRYQSHPDAAVQ 556
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 10

ABU04716
ID ABU04716 standard; protein; 556 AA.
XX
AC ABU04716;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1382.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1382; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The

PS Example 2; SEQ ID NO 1378; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents a
CC expressed protein tag (SPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SO Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPSMVRTQTSSTPPGIPGGSROGPAMDQTAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPSMVRTQTSSTPPGIPGGSROGPAMDQTAAPRP 60
Oy 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDEKLYFGLSYAKNGSLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDEKLYFGLSYAKNGSLKYIRKIGSFDET 180
Oy 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINILLNEDMHIQITDPTAKVLSPEKQARAN 240
Oy 241 SPVGTQAYVSPPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTQAYVSPPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDAITRLGCEMBGYGGLKAHPPFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDAITRLGCEMBGYGGLKAHPPFESVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDSDCYGNYDNLSSQPGCMQVSSSSSSSLASDGLPQRSGSNIEQYIHDLQ 420
Db 361 YLPAMSEDDSDCYGNYDNLSSQPGCMQVSSSSSSSLASDGLPQRSGSNIEQYIHDLQ 420
Oy 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480

CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SO Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPSMVRTQTSSTPPGIPGGSROGPAMDQTAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPSMVRTQTSSTPPGIPGGSROGPAMDQTAAPRP 60
Oy 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDEKLYFGLSYAKNGSLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDEKLYFGLSYAKNGSLKYIRKIGSFDET 180
Oy 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINILLNEDMHIQITDPTAKVLSPEKQARAN 240
Oy 241 SPVGTQAYVSPPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTQAYVSPPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFFPKARDLVEKLLVLDAITRLGCEMBGYGGLKAHPPFESVTWENLHQOTPPKLT 360
Db 301 FPEKFFPKARDLVEKLLVLDAITRLGCEMBGYGGLKAHPPFESVTWENLHQOTPPKLT 360
Oy 361 YLPAMSEDDSDCYGNYDNLSSQPGCMQVSSSSSSSLASDGLPQRSGSNIEQYIHDLQ 420
Db 361 YLPAMSEDDSDCYGNYDNLSSQPGCMQVSSSSSSSLASDGLPQRSGSNIEQYIHDLQ 420
Oy 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPHQPVENNLI LKMGVVDKRGKLFARRRQLLLTE 480
Oy 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540
Db 481 GPHLYYVDVFNKVLKGSIPWSQELRPEAKNFKTFPVHTPNRTYYLMDPSGNAHKWCRKIQ 540

Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 11

ABU04711
ID ABU04711 standard; protein; 556 AA.
XX
AC ABU04711;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1377.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1377; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGSRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGSRQGPAMDGTAAAPRP 60
Oy 61 GAGSLQHAQPPQPRKQRPEDPKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPQPRKQRPEDPKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKGELLKYIRKIGSFDET 180
Oy 181 CTRPYTARIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTARIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240
Oy 241 SFVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SFVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFPFKARDLVEKLLVLDAITKRLGCEMGGYGLKAHPFESVTWENLHQTPPKLTA 360
Db 301 FPEKFPFKARDLVEKLLVLDAITKRLGCEMGGYGLKAHPFESVTWENLHQTPPKLTA 360
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHLSASDGTLPQSRGSGNIROYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHLSASDGTLPQSRGSGNIROYIHDL 420
Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLPARRRQLLTS 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLPARRRQLLTS 480
Oy 481 GPHLYYVDVNVKLVKGIIPWSQELSPAQNFKTFPVHTPNRTTYLADPSNAHHCWKRIQ 540
Db 481 GPHLYYVDVNVKLVKGIIPWSQELSPAQNFKTFPVHTPNRTTYLADPSNAHHCWKRIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 12

ABU04706
ID ABU04706 standard; protein; 556 AA.
XX
AC ABU04706;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1372.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1372; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGSRQGPAMDGTAAAPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTQTSSTPPGIPGSRQGPAMDGTAAAPRP 60
Oy 61 GAGSLQHAQPPQPRKQRPEDPKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Db 61 GAGSLQHAQPPQPRKQRPEDPKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYFGLSYAKGELLKYIRKIGSFDET 180
Oy 181 CTRPYTARIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTARIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240
Oy 241 SFVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SFVGTAAQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Oy 301 FPEKFPFKARDLVEKLLVLDAITKRLGCEMGGYGLKAHPFESVTWENLHQTPPKLTA 360
Db 301 FPEKFPFKARDLVEKLLVLDAITKRLGCEMGGYGLKAHPFESVTWENLHQTPPKLTA 360
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHLSASDGTLPQSRGSGNIROYIHDL 420
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHLSASDGTLPQSRGSGNIROYIHDL 420
Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLPARRRQLLTS 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLPARRRQLLTS 480
Oy 481 GPHLYYVDVNVKLVKGIIPWSQELSPAQNFKTFPVHTPNRTTYLADPSNAHHCWKRIQ 540
Db 481 GPHLYYVDVNVKLVKGIIPWSQELSPAQNFKTFPVHTPNRTTYLADPSNAHHCWKRIQ 540
Oy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 13

ABU04714
ID ABU04714 standard; protein; 556 AA.
XX
AC ABU04714;

XX
DT 29-JAN-2003 (first entry)
XX
DS Human expressed protein tag (EPT) #1380.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1380; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

5Q Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRQTESSTPPGIPOGSRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRQTESSTPPGIPOGSRQGPAMDGTAAEPRP 60
Qy 61 GAGSLQHAQPPQPQRKGRPEDFKPKILGEGSFSTVVLARELATSREYAIKILKSHI1K 120
Db 61 GAGSLQHAQPPQPQRKGRPEDFKPKILGEGSFSTVVLARELATSREYAIKILKSHI1K 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRLDKPENILLNEDMH1QITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRLDKPENILLNEDMH1QITDPTAKVLSPEKQARAN 240
Qy 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEEMGYPGLKHPFESVTWNHQQTPPKLTA 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEEMGYPGLKHPFESVTWNHQQTPPKLTA 360
Qy 361 YLPAMSEDDDCYGNNDNLSPQGMQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420
Db 361 YLPAMSEDDDCYGNNDNLSPQGMQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGVPDKRGLFARRRQLL 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGVPDKRGLFARRRQLL 480
Qy 481 GPHLYYVDPVNKLKGSIPWSQLRPEAKNFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540
Db 481 GPHLYYVDPVNKLKGSIPWSQLRPEAKNFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 14
ABU04707
ID ABU04707 standard; protein; 556 AA.
XX
AC ABU04707;
XX
DT 29-JAN-2003 (first entry)
XX
DS Human expressed protein tag (EPT) #1373.
XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1373; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRQTESSTPPGIPOGSRQGPAMDGTAAEPRP 60
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRQTESSTPPGIPOGSRQGPAMDGTAAEPRP 60
Qy 61 GAGSLQHAQPPQPQRKGRPEDFKPKILGEGSFSTVVLARELATSREYAIKILKSHI1K 120
Db 61 GAGSLQHAQPPQPQRKGRPEDFKPKILGEGSFSTVVLARELATSREYAIKILKSHI1K 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180
Qy 181 CTRFYTAIVSALEYLHGKGIHRLDKPENILLNEDMH1QITDPTAKVLSPEKQARAN 240
Db 181 CTRFYTAIVSALEYLHGKGIHRLDKPENILLNEDMH1QITDPTAKVLSPEKQARAN 240
Qy 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Db 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEEMGYPGLKHPFESVTWNHQQTPPKLTA 360
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEEMGYPGLKHPFESVTWNHQQTPPKLTA 360
Qy 361 YLPAMSEDDDCYGNNDNLSPQGMQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420
Db 361 YLPAMSEDDDCYGNNDNLSPQGMQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGVPDKRGLFARRRQLL 480
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGVPDKRGLFARRRQLL 480
Qy 481 GPHLYYVDPVNKLKGSIPWSQLRPEAKNFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540
Db 481 GPHLYYVDPVNKLKGSIPWSQLRPEAKNFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 15
ABU04717
ID ABU04717 standard; protein; 556 AA.
XX
AC ABU04717;
XX
DT 29-JAN-2003 (first entry)
XX
DS Human expressed protein tag (EPT) #1383.
XX

Query Match 100.0%; Score 2941; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.3e-249;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:31:32 ; Search time 42 Seconds
(without alignments)
1273.727 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIQSVWRQYQSHPDAAVQ 556

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	873.5	29.7	592	2	T43402	probable protein k
2	832	28.3	488	2	T48447	3-phosphoinositide
3	748.5	25.5	1081	2	S51899	probable protein k
4	733	24.9	550	2	T40485	phosphoinositide-d
5	712	24.2	766	2	S69657	hypothetical prote
6	648.5	22.1	898	2	S69634	hypothetical prote
7	606.5	20.6	893	2	S63378	hypothetical prote
8	568.5	19.3	648	1	JQ1150	protein kinase (EC
9	566	19.2	471	2	S68463	protein kinase ATP
10	565.5	19.2	320	2	T33662	hypothetical prote
11	565.5	19.2	465	2	S68462	protein kinase ATP
12	562.5	19.1	431	2	A48094	serum and glucocor
13	561.5	19.1	338	2	S00085	protein kinase (EC

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-592 <WOO>
A;Cross-references: UNIPARC:UPI0000069B00; EMBL:AL031798; PIDN:CAA21194.1;
GSPDB:GN00068; SPDB:SPCC576.15c
A;Experimental source: strain 972h-; cosmid c576
C;Genetics:
A;Gene: KSG1; SPCC576.15c
A;Map position: 3
A;Introns: 191/3
C;Keywords: phosphotransferase

Query Match 29.7%; Score 873.5; DB 2; Length 592;
Best Local Similarity 37.3%; Pred. No. 1.3e-29;
Matches 212; Conservative 89; Mismatches 166; Indels 101; Gaps 17;

Qy	14	IQSSVLLCSPSPSMVTRQTTSSTPPGIPGSGRQGPAMDGTAAAPRPGAGSLQHAQPPPP 73
Db	49	IPQSNALATTTPNESTQSDISSPKIPSAVP-----HISTPNPSSGA-----ST 90
Qy	74	PRKGRPEDFKFGKILGSGSFSTVLARSLATSRSAIKILEKRIHIIKENKVPVYTRERDV 133
Db	91	PNIKRVSDPKFGSILGGSYSTVLATENSTKREYAIKVLKRIHIIKEKKEKYNIEKEA 150
Qy	134	MSRLD-HPPFVKLYPTFQDDKLYPGLSYAKNGELLYKIRKIGSPDETCTRTFYARIVSA 192
Db	151	LCILSKHPGFIKLFYTPQDAHNLVYFVLSLARGNELLDYINKLGRFNSICAQYAAALVDS 210
Qy	193	LEYLHGKGIHRLDKPENILLNEDHGIQITPOTAKVLS-----PESKQARAN 270
Db	211	IDYHMGKGVIRDLKPENILLNEDHGIQITPOTAKVLS-----PESKQARAN 270
Qy	241	SFVGTAAQYVSPPELLTEKSAKSSDLALGCIYYQLVAGLPFRAGNEYLIPOKIKLEVD 300
Db	271	SFVGTARYVSPVELSDKIAGTASDIWAGCILFQMLAGKPPFVAGNEYLIPOKIKLEVD 330
Qy	301	PPSKFFPKARDLVKLLVLDATKRLGCEMBGYPGLKAPPPFESVTWEN-LHQOTPPKLT 359
Db	331	IPPDISDVASDLIKGLVLDPKDLTVDE-----LHGHPFGKIFDNTLWELPPRLK 384
Qy	360	AYLPAMSEDDSDCYGNVNDLLSGPQGVSSSSSSSS-----LSASTDGLQ 406
Db	385	PP-----GHTSVLS-----LSVPASNNHKGDLTSLPLGVPMKVSASTNAAPS 427
Qy	407	RSGSNIEQYIHLDLNSNFELOLQFS-----EDEK-----RLLEKQAG--GNPWHQPVENN 455
Db	428	PVOTFNRTGLLPCQSNLEBENKMSISLQDDSKISKIOTLVNYSMSGINGNDAPRPPSS- 486
Qy	456	LILMGVPDKKGLFARR--RQLLLTS-GPHLYYVD--PVNVLKGISP--MSQELRPE 507
Db	487	-----LFRKIKRPTFILTNGRYLCVASDGBGRVTKESIPKISVQMRCKV 533
Qy	508	AKNFKTFVHTPHRTTYLMDPSNAHW 535
Db	534	KNNHGMVVTPTKMSFEDPMPASAW 561

14	560.5	19.1	358	2	T38121	protein kinase - h
15	558.5	19.0	351	1	OKHYCB	protein kinase (EC
16	558.5	19.0	351	1	OKHSCB	protein kinase (EC
17	558.5	19.0	351	1	OKRCCB	protein kinase (EC
18	558.5	19.0	425	2	S41099	protein kinase (EC
19	557.5	19.0	351	1	OKBOB1	protein kinase (EC
20	557.5	19.0	371	2	T16391	hypothetical prote
21	557.5	19.0	397	1	OKBOB2	protein kinase (EC
22	557	18.9	334	2	A60543	protein kinase (EC
23	556	18.9	398	1	OKBYC3	protein kinase (EC
24	555	18.9	680	2	S37955	protein kinase YPK
25	554	18.8	380	1	OKBYC2	protein kinase (EC
26	553	18.8	502	2	F31751	protein kinase cat
27	550.5	18.7	351	1	OKHUCB	protein kinase (EC
28	548.5	18.7	312	2	T32446	hypothetical prote
29	548.5	18.7	312	2	A89460	protein H42K12.1 [
30	548	18.6	375	2	T21212	hypothetical prote
31	547.5	18.6	726	2	S22258	probable protein k
32	546.5	18.6	677	2	J50178	protein kinase YKR
33	546	18.6	351	1	OKBO2C	protein kinase (EC
34	545.5	18.5	1092	2	H96509	protein F27F5.23 [
35	544.5	18.5	360	1	OKHUCG	protein kinase (EC
36	543	18.5	359	2	T21211	hypothetical prote
37	542	18.4	351	1	OKHUC2	protein kinase (EC
38	541	18.4	351	1	OKHYCA	protein kinase (EC
39	541	18.4	375	1	OKHUC2	protein kinase (EC
40	540.5	18.4	569	2	T50414	probable prolifera
41	539.5	18.3	479	2	A38578	protein kinase 2 (
42	539.5	18.3	541	1	T43232	protein kinase (EC
43	538	18.3	351	1	OKM5CA	protein kinase (EC
44	538	18.3	480	2	S56639	ribosomal protein
45	537	18.3	351	1	OKRT2C	protein kinase (EC

ALIGNMENTS

RESULT 1

T43402
probable protein kinase (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43402; T41425
R;Niederberger, C.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z22486
A;Accession: T43402
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-592 <NIE>
A;Cross-references: UNIPROT:Q12701; UNIPARC:UPI0000069B00; EMBL:X99280;
PIDN:CAA67672.1
A;Experimental source: strain h90
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21954
A;Accession: T41425

RESULT 2

T48447
3-phosphoinositide-dependent protein kinase-1 PDK1 - Arabidopsis thaliana
N;Alternate names: protein T32M21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48447
R;Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De Keyser, A.; Neyt, P.; Rouse, P.; Van Den Daele, H.; Villarroel, R.; Gielen, J.; Van Montagu, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24487
A;Accession: T48447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <BEV>
A;Cross-references: UNIPROT:Q9LZ74; UNIPARC:UPI000009CS94; EMBL:AL162875
A;Experimental source: cultivar Columbia; BAC clone T32M21
C;Genetics:
A;Map position: 5
A;Introns: 54/3; 115/1; 132/3; 166/3; 203/1; 229/2; 284/3; 329/3; 387/2; 461/3
A;Note: T32M21.110

Query Match 28.3%; Score 832; DB 2; Length 488;
Best Local Similarity 40.2%; Pred. No. 5.6e-28;
Matches 192; Conservative 69; Mismatches 165; Indels 52; Gaps 11;

Qy	81	DPKPGKILGSGSFSTVLARSLATSRSAIKILEKRIHIIKENKVPVYTRERDVMSRLDHP 140
Db	40	DFSPGKIYGVGSGKRVRAKGGTGTOTVYALIKNDKPKITKMKTAIVKLERIVLDQLEHP 99
Qy	141	FPVGLYPTFQDDKLYPGLSYAKNGELLYKIRKIGSPDETCTRTFYARIVSAVLYHGK 200
Db	100	QIKLYPTFQDTSLLYALSCGGELPDQITKRGRLSEDEARPYTARVVDALSYIHSWG 159
Qy	201	IHRDLKPENILLNEDHGIQITPOTAKVLS-----VLPESKQARANSPVGTAAQYVSP 252
Db	160	IHRDLKPENILLNEDHGIQITPOTAKVLS-----VLPESKQARANSPVGTAAQYVSP 219
Qy	253	LLTEKSAKSSDLALGCIYYQLVAGLPFRAGNEYLIPOKIKLEVDPPKFKPKARDL 312
Db	220	VLNSSPATFGNDLWALGCTLYQMLSGTSPFKDASEWLPQRIIARDIKFNNHPSBAARDL 279
Qy	313	VEKLLVLDATKRLGCEMBGYPGLKAPPPFESVTWENLHQOTPPKLTAYLPA--MSDD 369
Db	280	IDRLDTPSPRRPGAGS-EGYVALKRXHPPNKGVDWNNRSQTPKLA-ADPAQATSPER 337
Qy	370	EDCYGNVNDLLSGPQGVSSSSSSSS-----LSASTDGLPQSGNSIEQYIHLDLNSNFE 426
Db	338	DDTHGSPWN-LTHIG-DSLATNGHGSAPPSSSSSSSITRLAS-----IDSFDSR-- 386
Qy	427	DLQPSDEKRLLEKQAGNPNHQPVE-NHLLMGVPDKKGLFARRRQLLLTEPHLY 485
Db	387	-----WQPLSGRSLVNIHSAVKQLKIKTSKXQVILTNKPKLI 425
Qy	486	YVDPVNVKLGKIPW--SQSLRPAKNTFTFVHTPHRTTYLMDPSNAHWCKRKIQ 540

Db 426 YVDPKLVKGNIIIMSDNSDLAVVVTSPSHFKICTPKKVLSPDAKQASVMKGAIE 483

RESULT 3

S51899

probable protein kinase HRC1081 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein Q0784; protein YOL100w
C:Species: *Saccharomyces cerevisiae*
C>Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C:Accession: S51899; S59175; S66796
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV
including the Ty1-H3 retrotransposon, the *sufl1(+)* frameshift suppressor gene for
tRNA-Gly, the yeast transfer RNA-Thr-1a and a Delta.
A:Reference number: S51848
A:Accession: S51899
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: UNIPROT:Q12236; UNIPARC:UP1000004F9FC; EMBL:Z48149;
NID:g663234; PIDN:CAA88162.1; PID:g663254
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A>Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
including the Ty1-H3 retrotransposon, the *sufl1(+)* frameshift suppressor gene for
tRNA-Gly, the yeast transfer RNA-Thr-1a and a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582
A:Accession: S59175
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: UNIPARC:UP1000004F9FC; EMBL:Z48149; NID:g663234;
PIDN:CAA88162.1; PID:g663254
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January
1995
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66791
A:Accession: S66796
A:Molecule type: DNA
A:Residues: 1-1081 <DUR>
A:Cross-references: UNIPARC:UP1000004F9FC; EMBL:Z74842; NID:g1419951;
PIDN:CAA99113.1; PID:e251892; PID:g1419952; MIPS:YOL100w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PKH2
A:Cross-references: SGD:S0005460
A:Map position: 15L
C:Keywords: ATP; phosphotransferase
F:177-443/Domain: protein kinase homology <KIN>
F:185-193/Region: protein kinase ATP-binding motif

Query Match 25.5%; Score 748.5; DB 2; Length 1081;
Best Local Similarity 38.1%; Pred. No. 3.2e-24;
Matches 164; Conservative 79; Mismatches 109; Indels 79; Gaps 11;

A:Cross-references: UNIPARC:UP1000006A777; EMBL:AL049489; PIDN:CAB39805.1;
GSPDB:GN00067; SPDB:SPBC1778.10c
A:Experimental source: strain 972h-; cosmid c1778
C:Genetics:
A:Gene: SPBC4C3.11; SPDB:SPBC1778.10c
A:Map position: 2
C:Keywords: phosphotransferase
Query Match 24.9%; Score 733; DB 2; Length 550;
Best Local Similarity 36.4%; Pred. No. 7.7e-24;
Matches 185; Conservative 82; Mismatches 165; Indels 76; Gaps 16;

Qy 77 KRPEDFKGKILGEGSFSTVVLARELATSREYAIIKILEKHHIIKENKVPVYTRERDVMS 136
Db 49 KSPADYVFGDIIGDGSFKVRRATDKGSKGYAIKVLIDKIVKENKVKYVNIERDSMOR 108
Qy 137 LD-HPPFVKLYPTFQDDSKLYPLGSYAKNGLLKIRKIGSPDSTCTRPYTAISIVSALEY 195
Db 109 LMGPGIISRLPHTFQDDSKLYPLGSYAKNGLLKIRKIGSPDSTCTRPYTAISIVSALEY 168
Qy 196 LHGKGIHRLDKPENILLNEDMHQIQTDPOTAKVLSPEKQAR-----ANSFVGTAYQVS 250
Db 169 MHSOGIHRDLKPENILFDGNGHIVKIDTPTAKILPPKYVNSPDYTFPSSFGVTAISYA 228
Qy 251 PELLTEKSACKSSDDLWALGCIYIQLVAGLPPFRAGNEYLFQKIHKLEYDFPEKFPFKAR 310
Db 229 PELLRSOVVSKSSDDLWAFACVYQIMVGSPPPHGSPNNPKIKIMSLEYELPKLLPDPDV 288
Qy 311 DLVEKLLVLDATKRLGCEEMGYPGLKAPHPFSSVTWNLHQOTPPKLTAYLPAMSEDD 370
Db 289 PLPSHLFRIQPSDRSTTQD-----IKOPFFATITWDLNLTQDPPFMQSRP----- 335
Qy 371 DCYGYND-----NLLSQFGQCMQVSSSSSHLSASDTGLP---QRS 408
Db 336 ---NYNIAIPNAPAYRSNVTAAAAAANAAP---ASASIVHQETARRQELPTVNRP 387
Qy 409 GSNIRQYIH-DLDSNSFELDQFSB---DSKRLLEKQAGNPHQFVNNLILKMGVPD 464
Db 388 TAPTAHYGASLRSQMPVDRILYKLVPSSESIESTSVFSPIPSPVSGNQV---PSG 443
Qy 465 KRKGLFARRRQ---LLTE-----GPH---LYYDVVNKVLKGSIPWSQSLRPAKQV 511
Db 444 LSK-MFLKQKQRMVLLTDVGRCAFVCKQKHEKLFIEKSVN---LKDS---SVVYFDENSS 497
Qy 512 KTFPVHTPNRTYLLMDPSNGAHQCKKI 539
Db 498 KRFLIEDKQVSWIIRDSGQVTKYDKKI 525

RESULT 5

S69657

hypothetical protein YDR490c - yeast (*Saccharomyces cerevisiae*)
C:Species: *Saccharomyces cerevisiae*
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C:Accession: S69657
R:Dietrich, F.S.
submitted to the EMBL Data Library, August 1995

Qy 76 KRPEDFKGKILGEGSFSTVVLARELATSREYAIIKILEKHHIIKENKVPVYTRERDVMS 135
Db 173 KKGIDKDFKQSGVIGGAYSTVHLATSIDTKGRVAAKVLKSEYLRQKKVKYVSISKATLG 232
Qy 196 LRDH-PPFVKLYPTFQDDSKLYPLGSYAKNGLLKIRKIGSPDSTCTRPYTAISIVSALE 194
Db 233 KLNNSPVVRLFTSFQDESSLYFLLEYAFNKGDFLSLAKKYGSLDCTARYAAGIIDAID 292
Qy 195 YLHGKGIHRLDKPENILLNEDMHQIQTDPOTAKVLSPEK-----QARANSFVGT 245
Db 293 YLHSGIHRDLKPENILLDGBMKIKLTDPTAKLNPNTNSVSKPEYDLSTRSKSPVOT 352
Qy 246 AQYVPELLTEKSACKSSDDLWALGCIYIQLVAGLPPFRAGNEYLFQKIHKLEYDFPEKFP 305
Db 353 ASYVPELLADSPTDYRCIDIMAFQCIILFQKLAGKPPFKATNSYLTPOKVMKQYAFTPGF 412
Qy 306 FPKARDLVKLLVLDATKRLGCEEMGYPGLKAPHPFSSVTWNLHQOTPPKLTAY-L 362
Db 413 PLIIRDLVKKILVKNLDRRLTIQ-----IKGHHFFKDLNFKDGSVMSKTPPEIKPYKI 466
Qy 363 PAMSEDDSDCYQNYNLLSQFGQCMQVSSSSSHLSASDTGLP---LQPSGS---NIR 413
Db 467 NAKS-----MQAMPQSGDRKLVKSVNLTGKSHLVTRQSASSPSVB 507
Qy 414 QYIHDLDSNSFELDQFSB---DSKRLLEKQAGNPHQFVNNLILKMGVPD----- 465
Db 508 ETTHTSTLVN-----NHTASTSESIISIKRPTDSRTAQILEN 544
Qy 466 -RKGLFARRRQ 475
Db 545 ARKGINNRKNQ 555

RESULT 4

T40486

phosphoinositide-dependent protein kinase 1 (EC 2.7.1.-) SPBC4C3.11 [imported] -
fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T40486; T39692
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.;
Dueterhoeft, A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21910
A:Accession: T40486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KOO>
A:Cross-references: UNIPROT:Q9Y7J6; UNIPARC:UP10000069850; EMBL:AL021730;
PIDN:CAA16833.1; GSPDB:GN00067; SPDB:SPBCAC3.11
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21869
A:Accession: T39692
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 385-550 <OLI>

A:Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69557
A:Molecule type: DNA
A:Residues: 1-766 <DIE>
A:Cross-references: UNIPROT:Q03407; UNIPARC:UP1000006A3C7; EMBL:U33050;
NID:g927726; PIDN:AAB64917.1; PID:g927745; MIPS:YDR490c
C:Genetics:
A:Gene: SGD:PKH1
A:Cross-references: SGD:S0002898
A:Map position: 4R
C:Keywords: ATP
F:123-391/Domain: protein kinase homology <KIN>
F:131-139/Region: protein kinase ATP-binding motif

Query Match 24.2%; Score 712; DB 2; Length 766;
Best Local Similarity 30.3%; Pred. No. 7.7e-23;
Matches 187; Conservative 87; Mismatches 154; Indels 190; Gaps 15;

Qy 27 SMVKTQTESSTPPGIPQSGRQ-----PANQGT-----AASPRGAAGSLQH 67
Db 22 SAETHTQGYPRPVDGNSNSQSGSELAQSPQOGFGKALSTNRPILANDDPP---MQH 78
Qy 68 AQP-PPQPRKQKPE-----DKFKGKILGSGSFST 95
Db 79 EMGLDPSMRRRRRBNASGAAKIVQDVDPATSLTGHVVMQIKDFPKGEGLDQSGYSS 138
Qy 96 VVLARELATSREYAIIKILEKHHIIKENKVPVYTRERDVMSRLDHPFFV-KLYPTFQDDSK 154
Db 139 VVLATARDSGKKYAKVLSKYLIRQKKVKYTVVEKLALQKLGNTGIFKLPFTFQDSAS 198
Qy 155 LYFLGSYAKNGLLKIRKIGSPDSTCTRPYTAISIVSALEYLHGKGIHRLDKPENILLN 214
Db 199 LYFLLEYAPHGDFLGLKIKYGSLSNCTARYASQIDAVDSLWNIQIHRDLKPENILLD 258
Qy 215 EDKHIQTDPOTAKVLSPEKQ-----ARANSFVGTAYQVSPELLTEKSACKSS 263
Db 259 KMKVKLTDPTAKILPSEPSNTADGKPYDYLAKSSEFVGTATSVYPELLANDNYDSRC 318
Qy 264 DLWALGCIYIQLVAGLPPFRAGNEYLFQKIHKLEYDFPEKFPKARDLVKLLVLDATK 373
Db 319 DIMAFGCILYQKLAGKPPKAAEYLFQKVMKIQYATGAPQIYKDLVKLLVRDPND 328
Qy 324 RLGCEEMGYPGLKAPHPFSSVTWNLHQOTPPKLTAY-----LPAMSEDD--- 369
Db 379 RLTIKQ-----IKAHLPFHEVNFEDGQVMDNPPRIOPYKINAEAMKPLQKVSSEDTTV 432
Qy 370 -----EDC 372
Db 433 KMANLQLAGNHADTPLQAAPASQHSVISMATAATAAPNKDYTSQPKLKSSTSVRSA 492
Qy 373 YGNVYDNLSSQFGQCMQVSSSSSHLSASDTGLPQPSGS---IEQYIHDLDSNSFELDQ 429
Db 493 SNNTDRVIVKQVSKNRSVSSPSTTTRGKNKRSSESDAPMSYRLQND----- 543
Qy 430 FSEDSKRLLEKQAG-----GNPHQFVNNLILKMGVPDKKQGL 469
Db 430 FSEDSKRLLEKQAG-----GNPHQFVNNLILKMGVPDKKQGL 469

```

Qy      407 RSGSNIEQYI-----HDLDSNSPELOLPSEDEK 435
          || | |           | : : : : : : |
Db      325 ----NIPONILPTROLHVIDTPARSIOITKOKKKK 355

```

RESULT 6

S69534
hypothetical protein YDR466w - yeast (*Saccharomyces cerevisiae*)
C:Species: *Saccharomyces cerevisiae*
C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C:Accession: S69534
R:Dietch, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of *S. cerevisiae* coamids 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69534
A:Molecule type: DNA
A:Residues: 1-898 <DIS>
A:Cross-references: UNIPROT:Q03306; UNIPARC:UPI000006C128; EMBL:U33055;
NID:g927726; PIDN:AAB64902.1; PID:g927730; MIPS:YDR466w
C:Genetics:
A:Cross-references: SGD:S0002874
A:Map position: 4R
C:Keywords: ATP
F:9-293/Domain: protein kinase homology <KIM>
F:17-25/Region: protein kinase ATP-binding motif

Query Match 22.1%; Score 648.5; DB 2; Length 898;
Best Local Similarity 37.7%; Pred. No. 3.8e-20;
Matches 149; Conservative 60; Mismatches 109; Indels 77; Gaps 10;

Qy	75	RKKRPEDPFKFKLIGSGSSYTVLVAR - LATSREYAKIKLEKRIHIIKKNVYVYTVRRFDV	133
Db	4	RKRSPHDPIFKESLGHGSSYTVFKALDKSPNKIYAKVKCSKGIHIIKSAKVYVYTIKOT	63
Qy	134	MSRL---DHPFVVKLYPTFODDEKLYPGLSYAKNGELLYIKRKISFDETCRTFYTAIV	190
Db	61	MTLLAQKHUAGIKLYPTFDESNELVYPLDPAFGKGLSLHKKQTFDITWRTHFAQLI	123
Qy	191	SALRYSLYKIIHRODKPENILNEDMGIITDPTGAKVSL---ESKQARA	249
Db	124	DALSFTHSHGIHRODKPENVLLDRDGLMIIDPGAATIDPSLSDSAKFNDSNGSKD	183
Qy	240	N---SPVGTQCYVSPELLTEKSACKSSDLMAWGCIYQVLVAGLPFFAGNSYLIPOKII	295
Db	184	WQNCASFVGTARVSPELLWQCCYGSIDLMAWGCMYQVQGGPPFRGNSLKTAKFIV	243
Qy	296	KLEYDF-----PKKFFPKARDVLEKLLVLDAIKRLGCESEMGYGLPKAHFFSVT	346
Db	244	ALDYPMGPNRNINNSTSPINPLVINLVKQILIVENNERISLQ-----IKRPYFVKD	297
Qy	347	WENLHQOTPPKLTAYLPAMSEDDDCGYNDNLISFGQCVSSSSSHSLSDGTLQD	406
Db	298	WN-----DKIKERHIGV-----SGGSLSGTLGLP---	352

RESULT 7

Hypothetical prote YNR047w - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N3449
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 05-Oct-2004
 C:Accession: 563378
 R:Pohl, T.M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: 563346
 A:Accession: 563378
 A:Molecule type: DNA
 A:Residues: 1-893 <POH>
 A:Cross-references: UNIPROT:P53739; UNIPARC:UPI000012DF15; EMBL:Z71662;
 MID:g1302557; PIDN:CAA96328.1; PID:e239836; PID:g1302558; MIPS:YNR047w
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0005330
 A:Map position: 14R
 C:Keywords: ATP
 F:494-777/Domain: protein kinase homology <KIN>
 F:502-510/Region: protein kinase ATP-binding motif

Query Match 20.6%; Score 606.5; DB 2; Length 893;
Best Local Similarity 31.7%; Pred. No. 2e-18;
Matches 155; Conservative 73; Mismatches 156; Indels 105; Gaps 14;

Qy	20	LCSCPSF---SWKRTTSTSTPPGIPGSGRGPAMQDAAEPFGAGSLQAHP-----P	72
Db	421	LASATSPTTSSARKTSGSSNINDKI PQGS-----VPPNSPFQPSPSKIDFP	469
Qy	73	QPRKKR-----PEDFGFKIGLGGSPSTVLARELATSREYAIKILEK	115
Db	470	EPKRSRLRLTKSPFNKQDINVGPQSPFKILRLGGQGVGVFLVREKKNRVLKVLKSL	529
Qy	116	RHIIKENKIVPVYTERDRSSDHLDPFKVLYPTTQDSKLYGLSVAGKGLLYI--RK	173
Db	535	DEMIRKKNIKRVLTQSILATSNHPIVTLVYHSPQSDYLYLQYCHYCHGSGFFRALQTRK	589
Qy	174	IGSFDTCTFTFYASIVSALEYLHGKGI IHRDLKPNKINLLNDSHQIGITDF-----	224
Db	590	TKCICEDDARFYASIVSALEYLHLLGFIYRLDKPNKINLLHSGSHIILSDPDLISQAKDS	649
Qy	225	-----GTAKVLSPEKKA-----RANSFVGTQAQVSPBLLETKSACKSSDLWALGCI IYO	274
Db	650	KVPVVGKSAQSTLVDTKICSDGFRTNFVGTGSEYIAPESIRNGKHTAADVMTLGIILYE	709
Qy	275	LVAGLPPFRGNGEYLI PQKIKILEYDFF---EKFFPKARDIVEKLLVLDATKRLGCSMSG	332
Db	710	MLPQFTPTPKQDMNTPTNLIKLGKTPVSPHNNISRTCDKILGLTKRSGKRLCK--MG	767
Qy	373	YGPLKAHFPSTVSTNMLHQQTPKPLTATLPAKSSDDEDCYQGNLDLNSGFGQVSSSS	392

Db 768 AADVKGIGPPFKVKKVSSLLNNSPP-----LIPVLSGSDGYFAKLSNKKR-----TSQ 816
 Qy 393 SSSHSLSASDTQLPQSGSNTGYHIDLDNSF-----ELDQPSSEKSKLLKKAQGNFW 448
 Db 817 DSH-----KHLDEQKQNFSEFSEVYDDEVSEDD-----PF 846
 Qy 449 HQFVNNLI 457
 Db 847 HDPFMSML 855

RESULT 8

JQ1150
 protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold
 (Dictyostelium discoideum)
 C:Species: Dictyostelium discoideum
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: JQ1150
 R:Buerki, B.; Anjard, C.; Scholder, J.C.; Raymond, C.D.
 Gene 102, 57-65, 1991
 A:Title: Isolation of two genes encoding putative protein kinases regulated
 during Dictyostelium discoideum development.
 A:Reference number: JQ1150; MUID:91323730; PMID:1864510
 A:Accession: JQ1150
 A:Molecule type: DNA
 A:Residues: 1-648 «BUE»
 A:Cross-references: UNIPROT:P34099; UNIPARC:UPI000012DC1F; GB:M38703
 C:Genetics:
 A:Gene: PK2
 A:Introns: 578/3
 C:Complex: heterodimer with regulatory chain; active catalytic chain is released
 when cAMP binds to the regulatory chain
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-
 threonine-phosphate using ATP
 A:Note: important for cell type differentiation and fruiting body morphogenesis
 C:Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain;
 protein kinase homology
 C:Keywords: ATP; magnesium; phosphoprotein; phosphotransferase;
 serine/threonine-specific protein kinase
 F:126-223/Region: glutamine-rich
 F:297-312/Region: glutamate-rich
 F:334-590/Domain: protein kinase homology «KIN»
 F:342-350/Region: protein kinase ATP-binding motif
 F:365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
 F:464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 19.3%; Score 568.5; DB 1; Length 648;
Best Local Similarity 36.7%; Pred. No. 5.7e-17;
Matches 115; Conservative 68; Mismatches 113; Indels 17; Gaps 4;

Oy 70 P P P Q P K I C R P S D F K F G K I L G E S F S T V V L A R E L A T S R E Y A I K I L E K R H I I K E N K V P Y V T R 129
 :
Db 124 P P P V N A R E L L G S F K Q I R V L O T O T F G K Y L I O N T K D C Y T A M K C L A H A V V Q L K Q V H S A S 383

Oy 130 R R D V M S R L D H P F V K L Y P T F O D D E K L Y P L S Y A J N G E L L Y I R K I G S F D E T C T R F Y T A S I 189

RESULT 9

568463
protein kinase ATPK19 (EC 2.7.1.-) - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 05-Oct-2004
C:Accession: S68463
R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
PEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in *Arabidopsis thaliana*.
A:Reference number: S68462; MUID:95129712; PMID:7828736
A:Accession: S68463
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residue: 1-471 <N12>
A:Cross-references: UNIPROT:Q93030; UNIPARC:UPI000016DAAE; EMBL:D42061;
H:1252641; PDB:1S6656;1; PDB:1S6656;1; PDB:1S6656;1
C:Keyword: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:138-395/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match 19.2%; Score 566; DB 2; Length 471;
Best Local Similarity 32.7%; Pred. No. 5.4e-17;
Matches 128; Conservative 79; Mismatches 142; Indels 42; Gaps 9;

Qy 15 QSSVLLGCLCPSPKSWRTQTSSTPPGIPQGRSQGPAMQDTAAEPSP-----GAGSLQHAQP 70
Db 156 EDSVQLVCEVGEGRSINKENDEFS-----GNDQDSGRSKPESVSGVGI----- 137

Qy 71 PPOPRKKRPPDFKFGKILGEGSPSTVLAELRATSREYAIKILSKKHIIKENKVPVYTR 130
Db 138 -----SDPEFLKVVQGAAGPVGVGVKRDSSIIYANKVWRKDKIKVGNHASYHKA 168

Qy 131 RDNVSRDLNHPFVKVLYPTFDQDSKLYPGLSYAKMKLLKIKIGSGFDSTCTAPTYTA 190
Db 139 RPIITKIDHPFIVQLVSEYQTKYKIVLVDPENIGHGLFPQIVHGLFPEVGVVYATVIR 246

[illegible]

Qy 72 POPRIQRQGFDPKGIKLGDSFPTVWLARELATSRYSATIKILSHHIIKBNKVPTVTRSR 131
Db 21 PAPINAGLSDPERIKVTGLTGSFGRVMLVHKHATCTYAMKILDXQVVKVWKQIISHTLNEK 80

Qy 182 DVMSRLDHPFVVKLYPTFQDDSKILYFGLSYANGSLLKYIRKIGFSDBTCTRPYATISVS 191
Db 181 RLQAVNPPKILVGLDFSPKNSHILVMYGVYQDGFPSHLRLGFPSEPHARYAAGIVL 140

Qy 182 ALRYAVHGGIKIINRDLKNSIIILNDDHVIITDPTTAVLAPSPSVAANSPVATQVPSR 250
Db 181

Db 141 TPFLHSLDLIYRDLKPENLLIDHQYIQVDPGFAGRV-----KQRTWLTQTPSYLAP 195
 Qy 252 ELLTEKSACKSSDLALGCIYYQLVAGLPPFRAGNEYLIPQKI I KLEYDPPKFPFKARD 311
 Db 196 EILLSKGYNKAVDMALGVLIYSMAAGYPPFPADQPIQIYKIVSGKVRPSPHSSDLKD 255
 Qy 312 LVEKLLVLDAIKRLGCEMSGYPLKAHPFFESVTWENLHQQTTPPKLTA-YLPAM-SEDD 369
 Db 256 LLRNLLQVLDLTKRFG-NLKNQVSDIKTHKWFATTDMIAIYQR---KVEAPFIPKFRGSD 311
 Qy 370 EDCYGNVD 377
 Db 312 TSNFDYD 319

RESULT 14

I38121
 protein kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I38121
 R:Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.; Ludecke, H.J.; Claussen, U.; Scherer, G.; Rappold, G.
 Hum. Mol. Genet. 4, 869-878, 1995
 A>Title: The human protein kinase gene PKI1 on Xp22.3 displays Xp/Yp homology and is a site of chromosomal instability.
 A:Reference number: I38121; MUID:95360006; PMID:7633447
 A:Accession: I38121
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-358 <RES>
 A:Cross-references: UNIPROT: P51817; UNIPARC: UP1000000D998; EMBL: X85545; NID: g1052736; PIDN: CAA59733.1; PID: g1052737
 C:Genetics:
 A:Gene: PKI1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 F:47-303/Domain: protein kinase homology <KIN>

Query Match 19.1%; Score 560.5; DB 2; Length 358;
 Best Local Similarity 36.6%; Pred. No. 7.2e-17;
 Matches 123; Conservative 63; Mismatches 119; Indels 31; Gaps 6;

Qy 37 TTPGIPGSGROGPMADGTAAEPGRAGSLQHAQPPQPRKPKRPEDFKFGKILGEGSFSTV 96
 Db 23 TPDGAP-----ALCPSPREALS-----PEPPVYSLQDPDTLATVGTGTGVRV 63
 Qy 97 VLARELATSREYAIKILEKRHIKENKVPYVTRERDMSRLDHPFVKLYPTFQDDSKLY 156
 Db 64 HLVEKTAIGHFFALKVMSIPDOVIRKQEQHVNHSKSVLKEVSHPLIRLPWTHDSRFLY 123
 Qy 157 FGLSYAKNGELLYIRKIGSFDETCTFRPYTASIVSALSYLHGKGIHRDLKPENILLNED 216
 Db 124 MLMEYVPGSLPSYLRNKRGRFSTTGLFYSAEIIICALSYLHSGKIVYRDLKPENILLDRD 183
 Qy 217 MHQITDPTGAKVLSPEKQARANSFVGTAAQYVSPPELLTEKSACKSSDLALGCIYYQLV 276
 Db 113 TPNLHSLDLIYRDLKPENLLIDHQYIQVDPGFAGRV-----KQRTWLTQTPSYLAP 208

Qy 72 POPRKRKRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIKENKVPYVTRER 131
 Db 34 PPPSNAGLSEDFSRKKTLTGTSFGVRMLVKHATQYVAMKILDKQKVVVLKQIEHTLNEK 93
 Qy 132 DVMSRLDHPFVKLYPTFQDDSKLYPGLSYAKNGELLYIRKIGSFDETCTFRPYTASIVS 191
 Db 94 RILQAVEPPFLVRLSEYFKDMSLVMYBYPVGGEMPSHLRIRGRFSPHARFYAAQIVL 153
 Qy 192 ALSEYLHGKGIHRDLKPENILLNEDMHQITDPTGAKVLSPEKQARANSFVGTAAQYVSP 251
 Db 154 TFEYHSLDLIYRDLKPENLLIDHQYIQVDPGFAGRV-----KQRTWLTQTPSYLAP 208
 Qy 252 ELLTEKSACKSSDLALGCIYYQLVAGLPPFRAGNEYLIPQKI I KLEYDPPKFPFKARD 311
 Db 209 EILLSKGYNKAVDMALGVLIYSMAAGYPPFPADQPIQIYKIVSGKVRPSPHSSDLKD 268
 Qy 312 LVEKLLVLDAIKRLGCEMSGYPLKAHPFFESVTWENLHQQTTPPKLTA-YLPAM-SEDD 369
 Db 269 LLRNLLQVLDLTKRFG-NLKNQVSDIKTHKWFATTDMIAIYQR---KVEAPFIPKFRGSD 311
 Qy 370 EDCYGNVD 377
 Db 325 TSNFDYD 332

Search completed: June 27, 2006, 01:37:05
 Job time : 44 secs

Db 184 GHIKLTPDGFAGKLVQ-----RTMTLOOTPSYLAPEVIQSKHGRAVDMALGILIPFML 238
 Qy 277 AGLPPFRAGNEYLIPQKI I KLEYDPPKFPFKARDLVEKLLVLDAIKRLGCEMSGYPL 336
 Db 239 SGPPFPFDNPPGIYQKILAGKIDFFRHLDPHVKDLIKLLLVORTERLG-NMUKGANDV 297
 Qy 337 KAHPPFESVTWENLHQQ--TPPKLTAYLPAMSEDD 370
 Db 298 KHRWFRSVQVAVPQRKLKP-----IVPKIAGDGD 329

RESULT 15

OKHYCB
 protein kinase (EC 2.7.1.37), cAMP-dependent, beta catalytic chain - Chinese hamster
 C:Species: Cricetus griseus (Chinese hamster)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A40384
 R:Howard, P.; Day, K.H.; Kim, K.B.; Richardson, J.; Thomas, J.; Abraham, I.; Fleischmann, R.D.; Gottesman, M.M.; Maurer, R.A.
 J. Biol. Chem. 266, 10189-10195, 1991
 A>Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA structure in a cAMP-resistant Chinese hamster ovary cell line.
 A:Reference number: A40384; MUID:91244783; PMID:1645343
 A:Accession: A40384
 A:Molecule type: mRNA
 A:Residues: 1-351 <HOW>
 A:Cross-references: UNIPROT: P05206; UNIPARC: UP1000000408F; GB: M63312; NID: g191176; PIDN: AAA37011.1; PID: g191177
 C:Comment: The inactive enzyme contains two regulatory chains and two catalytic chains. Activation by cAMP produces two active catalytic monomers and a regulatory dimer that binds four cAMP molecules. Two types found in mammalian tissue are distinguished by having either type I or type II regulatory chains.
 C:Comment: Both alpha and beta catalytic chains are found in many tissues, with the alpha form being the more abundant. The highest concentrations of the beta form are found in brain.
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; blocked amino end; cAMP binding; heterotetramer; lipoprotein; magnesium; myristylation; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F:2-351/Product: protein kinase, cAMP-dependent, beta catalytic chain #status predicted <MAT>
 F:42-298/Domain: protein kinase homology <KIN>
 F:50-58/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Modified site: aspartic acid (Asn) #status predicted
 F:55,56,122,128,171,184/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Thr) #status predicted
 F:73,92,167,169/Active site: Lys, Glu, Asp, Lys #status predicted
 F:172,185/Binding site: magnesium (Asn, Asp) #status predicted
 F:198/Binding site: phosphate (Thr) (covalent) #status predicted
 F:339/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 19.0%; Score 558.5; DB 1; Length 351;
 Best Local Similarity 36.7%; Pred. No. 8.5e-17;
 Matches 113; Conservative 66; Mismatches 118; Indels 11; Gaps 5;

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Perfect score: 2941
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	1367	46.5 687 6	US-10-449-902-53930 Sequence 53930, A
2	812	27.6 498 6	US-10-449-902-51984 Sequence 51984, A
3	736.5	25.0 417 6	US-10-449-902-33335 Sequence 33335, A
4	561	19.1 431 6	US-10-505-928-845 Sequence 845, App
5	561	19.1 431 6	US-10-472-622A-2 Sequence 2, Appli
6	558	19.0 480 6	US-10-449-902-50842 Sequence 50842, A
7	551	18.7 340 6	US-10-953-349-17750 Sequence 17750, A
8	551	18.7 418 6	US-10-953-349-17749 Sequence 17749, A
9	551	18.7 479 6	US-10-953-349-17748 Sequence 17748, A

; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53930
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53930

Query Match 46.5%; Score 1367; DB 6; Length 687;
Best Local Similarity 51.3%; Pred. No. 1.8e-60;
Matches 278; Conservative 74; Mismatches 120; Indels 70; Gaps 6;

Oy 76 KQRPEDFKGKILGSGSFSTVVLARELATSREYAIKILSKRHIIKENKVPVYTRERDVM 135
Db 141 KRSPNDPIFGKTIIGSGSPSSVYLAKDHTNKGYAIKVCDKRIHIREKKTEYVKLSKEVLM 209
Oy 136 RLDD-----PPFVKLYFTPDDEKLYFGLSVAKNGELLKYIRKIGSFDETCRFTYAI 189
Db 201 ILSNSNFIAPFPVKLCTFODARLFPVLYTAKNGELLPIYINKVGSFDIACSRFTYAI 260
Oy 190 VSALEYLHGKGIHRLDKPENILNEDMHIIQITDFTAKVLSPE-----SKQARA 239
Db 261 IMALEHMLRLRIHRLDKPENILNEDMHILVDFQSAKILPPEQPKDEVDGKVTRESRR 320
Oy 240 NSFVGTATQVSPPELLTEKSACKSSDLALALGCIYQVLVAGLPPFRAGNEYIFOKIKLEY 299
Db 321 NSFVGTATQVSPPELLTEKSACKSSDLALALGCIYQVLVAGLPPFRAGNEYIFOKIKLEY 380
Oy 300 DFPKFFPKARDLVSKLLVLDATKRLGCEM--EGYPLKHPFFESVTWENLHQOTPPK 357
Db 381 EFPDGFPLARDLVSKLLVLDATKRLGCEM--EGYPLKHPFFESVTWENLHQOTPPK 440
Oy 358 LTAYLPAMSEDE-----DCYGNYNLLSQFGCMQ 387
Db 441 ILPYLPOTSEELRSQYRVPDHLPEGLDRQLTRLLQLQLSQSGNSGNSGSSGSSN 500
Oy 388 VSSSSSSSHLSASDTGLPQRSQS-----NIGQYIHLDSNPFSLDLPQSEDEKRR- 436
Db 501 TSSSCSSSSSERTPEANPRKASPOPGPAPTDRDKRDKAKESARESTRAAQRORD 560
Oy 437 -----LILSKQAGGNPHQFVNNILILQGVVDKRGKLFARRRQLLTTEPHLY 485
Db 561 KLPNYSPEQALIQDRQARENQHPVNNILILQGVVDKRGKLFARRRQLLTTEPHLY 620
Oy 486 YVDPVNVKVLKGIIPMSQSLRPEAKNFTPTFVHTPNRTYLYKOPSGNAHMKCRKORVMRQ 545
Db 621 YVDPVNVKVLKGIIPMSQSLRPEAKNFTPTFVHTPNRTYLYKOPSGFALDWCVIISGRK 680
Oy 546 RY 547
Db 681 TY 682

RESULT 2
US-10-449-902-51984
; Sequence 51984, Application US/10449902

10 550.5 18.7 351 6 US-10-505-928-658 Sequence 658, App
11 544.5 18.5 693 6 US-10-449-902-37629 Sequence 37629, A
12 544 18.5 580 6 US-10-449-902-41431 Sequence 41431, A
13 537.5 18.3 485 6 US-10-449-902-44100 Sequence 44100, A
14 526.5 17.9 706 6 US-10-511-937-2450 Sequence 2450, App
15 512.5 17.4 556 6 US-10-449-902-54017 Sequence 54017, A
16 512.5 17.4 685 6 US-10-449-902-37624 Sequence 37624, A
17 512 17.4 480 6 US-10-511-814-6 Sequence 6, Appli
18 512 17.4 480 7 US-11-289-102-325 Sequence 325, App
19 509 17.3 616 6 US-10-449-902-44738 Sequence 44738, A
20 508.5 17.3 544 7 US-11-293-697-3334 Sequence 3334, App
21 502 17.1 733 6 US-10-505-928-349 Sequence 349, App
22 490 16.7 630 7 US-11-293-697-3776 Sequence 3776, App
23 478.5 16.3 310 6 US-10-449-902-33480 Sequence 33480, A
24 478.5 16.3 451 6 US-10-449-902-47001 Sequence 47001, A
25 474.5 16.1 451 6 US-10-449-902-44457 Sequence 44457, A
26 468.5 15.9 498 6 US-10-953-349-3867 Sequence 3867, App
27 468.5 15.9 519 6 US-10-953-349-3866 Sequence 3866, App
28 468.5 15.9 563 6 US-10-953-349-3865 Sequence 3865, App
29 463.5 15.8 592 6 US-10-505-928-146 Sequence 146, App
30 462 15.7 587 6 US-10-953-349-17119 Sequence 17119, A
31 462 15.7 674 6 US-10-953-349-17118 Sequence 17118, A
32 456 15.5 408 6 US-10-953-349-17120 Sequence 17120, A
33 454 15.4 434 6 US-10-449-902-45070 Sequence 45070, A
34 454 15.4 457 6 US-10-449-902-54251 Sequence 54251, A
35 454 15.4 465 6 US-10-953-349-20724 Sequence 20724, A
36 454 15.4 483 6 US-10-953-349-20723 Sequence 20723, A
37 454 15.4 503 6 US-10-953-349-20722 Sequence 20722, A
38 453.5 15.4 542 7 US-11-090-689B-3 Sequence 3, Appli
39 452 15.4 782 6 US-10-449-902-42854 Sequence 42854, A
40 451 15.3 459 6 US-10-953-349-38583 Sequence 38583, A
41 450 15.3 451 6 US-10-953-349-38584 Sequence 38584, A
42 450 15.3 502 6 US-10-449-902-55917 Sequence 55917, A
43 450 15.3 574 6 US-10-449-902-38154 Sequence 38154, A
44 450 15.3 574 6 US-10-449-902-50422 Sequence 50422, A
45 447.5 15.2 344 6 US-10-505-928-387 Sequence 387, App

ALIGNMENTS

RESULT 1
US-10-449-902-53930
; Sequence 53930, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205YI-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870

; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205YI-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51984
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51984

Query Match 27.6%; Score 812; DB 6; Length 498;
Best Local Similarity 37.6%; Pred. No. 2e-33;
Matches 198; Conservative 74; Mismatches 189; Indels 66; Gaps 13;

Oy 50 AMDGTAAPRPGAGSILQHAQPPQPRK-----KRP-----DPKFGKILGSGS 92
Db 2 AVGGDDMERDFAARLRAPSPASPAAGGGGGIAFRAPQEQVTPVDFELGKIYGVGS 61
Oy 9 FSTVVLARELATSREYAIKILSKRHIIKENKVPVYTRERDVMRLDHPFVKLYFTFDD 152
Db 62 YSKVRAKKKDTGNVYALKIMDKKPIYKNIKYVYKSRIVLQDLDPVIRLPTFTDPT 121
Oy 153 EKLFGLSYAKNGELLKYIRKIGSFDETCRFTYAIISVALSYLHGKGIHRLDKPENIL 212
Db 122 YSLYALBSCEGSLFDQIVKRGKLSDEBARPTAASIVDILSYLHSLGLIHRYKVENIL 181
Oy 213 LNEDMHIIQITDFTAK-----VLSPEKQARANSFVGTATQVSPPELLTEKSACKSSDL 265
Db 182 LTSGHIKIADSGSVKPTKDTPIKVLNPSINERACTFVGTATQVSPPEVLSAPPFTGIDL 241
Oy 266 WALOCIYQVLVAGLPPFRAGNEYIFOKIKLSDYFSPKFFPKARDLVKLLVLDATKRL 325
Db 242 WALGCTLYQLGSGSPFKASDLWIFORIARDLRIPEYFSDARDLIDKLDVDPKRP 301
Oy 326 GCSSEMOYGLKHPFFESVTWENLHQOTPPKLTAYLPAMSEDEDCYGNYNLLSQFGC 385
Db 302 GAGP-DGVVSLKGGPPFRGIDMKNIRSTRAPKA--KEANANEDSDQS--SWLSHW- 355
Oy 386 MOVSSSSSHLSASDTGLPQRSQNTSEYIHLDSNPFSLDLPQSEDEKRLLESKQAG 444
Db 356 ---SAPNVQHVSPVNDG---ASSSESVRSIIRLSDISFD----- 391
Oy 445 GNPWHQFVNNI-----LILKQAGGNPHQFVNNILILQGVVDKRGKLFARRRQLLTTEPHLY 500
Db 392 -SRWDFLEPGSVVLISLKKINK--LTKIKVGLITDKPOLICYDPQIKVTKNIKW 447

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RESULT 7
US-10-953-349-17750
: Sequence 17750, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCES-DETERMINED DNA FRAGMENTS AND CORRESPONDING
POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1578PUS2

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Qy      76  WKGPDEFPKFKILBGSPSTVVLARELSATSYEYAKIKLSEKHNIKENKVYPTVRDVM 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      244  KVLRLDFELLKVLGRGSPGVKGVKKGTGKIFAMKILKQRAIIARNQVSTKASRKILQ 303

Qy      136  RLDPHFVFKLYPTFQDDKRLKYLGSYAKNGELLYIRKIGSPDSTCTPTASIVSALEY 195
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      304  ALQHPHMLDRLTAFPSSEKELLYVLLQYDQVGLGHPHLKNKRKPGEDVARIYVGEIAAAGH 363

Qy      196  LHGKIITFHTLAKPNIILNEDMHIQITDGTAKVLSPESKQARANSPTAQVYSPBLAT 255
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      364  LHSIGVIRYLDKIPNIILDDNGHVCLDTGLSKVDVPSDK--AHTFGTTPYLAPSIYT 420

Qy      256  EKSACKSSDLWALGCIYIQLVGLPPFRAGNEYLIKQIKLEYDPFEPFKPKARDLVEK 315
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      421  GAGHDKAVDWMSLIIYLYLFTVGIPPPYBQNVNSYNYKIGHVLRPPFPLSECKSLIVA 480

Qy      316  LLVLDTATRLGCEMEHYGPKLKAHPFSPSTWENLHQ---QTPPKLTAIYAMSSDDSDC 372
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      481  LLNRDPAKRLG--SGKLDLVKSHAPFKDLMDIQMKREIVP----YKPKYKSGDDT- 532

Qy      372  YGYNDNLISQFGCMQVSSSSSSSSLSASDTGLPQRSGNIIOYIHDLDNSFPELDQFSE 432
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Db      533  -QNPDSTPTKEPV--VDSHVPTSKLTETVTSNP-----DAPK-DPTFOQ 572

Qy      433  DEKRL 438
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Db      573  NSKIL 578

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Qy     136  QPRKQRPEDPFGFKILGSGSFVTLARLSATSREYAIKILEKHHIKNNKVPVYTRERD  13
Db     146  -----DDFSLILKLVQGGAGFVQVQRKGTSSIYANKVKKKMLIKLKGHSYHKAERD  198

Qy     204  VMSRLDHPHFFVLYPTFODDSLLKYFSGYANGSLKYIKRGISGTFCTPRTATVISA  192
Db     218  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  258

Qy     256  ILTKVDHPFVQGLRYSFQTKRLRLVLDPFINGHLPFQGLFRELARITTAIVISA  252
Db     270  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  310

Qy     320  LEYLHGKGIILHRLDKPFIILNEDHGHIQTDPGATKVLSPESKQARANSFVGTAQVSP  252
Db     334  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  374

Qy     388  VAHLNDNGIILHRLDKPFIILDADGHMLDTPGLAKGF-----NENTSRNSGCTVSMAP  315
Db     402  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  442

Qy     456  LLTEKSKASSDMLAGCIYIQLVAGLPPFRAGNYSLFQKILKLYLDPFKSKFFKARDL  312
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Db     538  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  578

Qy     592  VEKLLVLDTAKRLGCEEMSGYGP-----LKAHPFFSFVYWEHL-QQTPPKLTATLPAS  366
Db     606  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  646

Qy     660  LKGLLLKKGGRKLGS-----GGGSDSIKRYIWKLPINRKLQARQIQPSFRPHVSLGT  428
Db     674  -----LILKILKILKILKILKILKILKILKILKILKILKILKILKILKILKILK  714

Qy     728  SDDDDCYGNYD 377
Db     742  -----CIANFD 434

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Qy		3	R	T	S	O	L	V	A	D	P	I	G	S	V	L	C	S	P	S	M	V	R	T	O	E	S	T	P	P	O	I	P	O	G	S	R	G	P	A	X	O	T	A	B	-P	R	P	G		61							
Db			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:										
	Db	305	R	D	E	O	I	F	R	E	G	V	E	I	G	L	-	-	-	-	-	-	-	P	C	S	I	K	N	-	-	-	A	R	P	C	L	P	T	P	K	R	E	P	-	Q	O	I	S	W	S	P	L	D	E		352	
Qy		62	A	G	S	L	H	A	Q	A	P	P	O	P	R	K	K	R	-	-	-	-	-	-	E	D	F	K	P	K	I	L	O	G	S	T	F	T	V	L	A	R	E	L	S	T	R	E	V	A	I	K	I	L		113		
Db			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:										
	Db	353	V	D	I	O	C	H	L	-	P	E	P	L	A	N	K	R	P	S	L	Q	I	K	I	E	D	F	L	I	H	Q	L	K	G	S	F	G	K	V	L	A	S	F	K	T	N	O	P	F	A	I	K	A	L		411	
Qy		114	S	K	R	H	I	K	E	N	K	V	P	T	R	R	D	V	K	-	-	-	-	R	L	O	H	P	F	V	K	L	Y	T	F	O	D	D	E	K	Y	P	G	L	S	A	I	N	G	E	L	L	K	Y	I	R		172
Db			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:										
	Db	412	K	D	V	L	A	D	D	V	E	C	T	E	K	S	V	R	V	L	S	A	M	S	P	F	L	T	H	M	F	C	T	O	T	K	E	N	F	V	P	N	E	L	A	G	G	D	M	Y	H	I	Q		471			
Qy		173	K	I	G	S	P	D	S	T	C	T	P	T	A	S	I	V	S	A	L	S	Y	L	H	O	K	I	I	H	R	L	K	P	E	N	I	L	A	S	D	M	H	I	O	T	P	T	A	K	V	L	S	P		232		
Db			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:										
	Db	473	S	C	H	P	K	L	S	R	A	T	F	A	A	S	I	L	O	L	O	F	L	O	S	I	V	Y	R	D	L	K	L	H	I	L	O	D	G	H	I	K	I	A	D	P	O	K	I		529							
Qy		233	E	S	K	-	Q	A	R	A	N	S	F	T	A	O	T	V	A	P	L	E	T	K	S	A	C	D	M	A	L	G	I	C	I	Y	O	L	V	A	L	P	P	R	A	G	N	E	-		590							
Db			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:										
	Db	528	S	N	L	D	A	K	T	F	O	T	P	D	Y	I	A	P	I	L	O	O	K	Y	N	S	V	D	N	S	F	G	V	L	L	Y	E	N	L	G	O	S	F	H	O	O	R	E	L		588							

[illegible]

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Db      287 PDSSRLSSSALKRTQQBQLSHWQKRRMLAYSTVOTPDYIAPSVLLKNOYQMECDWMSL 346
Oy      269 GCIIYQLVAGLEPPFRAGNSYLIPOKII--KLEYDPPE--KFFPKARDLVEKLLVLDATKR 324
Db      347 GAINYEMLVQYPPFYSEDPMSTCRKIVNWRSHLQPPERAKLSPEAKDLISKLL-CNVEQR 405
Oy      325 LGCEMEGYGPLKAHPFFESVTWENLHQQTPPKLTAYLPAM-SEDDDCYGNYNLLSQF 383
Db      406 LG--TKGAHBIKAHPWFRGLPWERLYQMK----AAFIPSVNSELOTQNFEEKF--BT 454
Oy      384 GCMQVSSSSSS---HSLASADTGLPORSQSNIEQYIHDLSNSFELDLOFSEDEK---R 436
Db      455 GA-QIQSSSKSGPMRKMLPSKDANFVGYYTYKNFBIVNDESVAGIAELKKKSSKSKRPTIK 513
Oy      437 LLLKQAGGNP 447
Db      514 TLFESMDEDS 524

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